

2) INFORMATION FOR SEQ ID NO: 2117

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2117

GCGGGCGACG CCATTGAGCC ACCTTCGAGA GCCCGC

36

2) INFORMATION FOR SEQ ID NO: 2118

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2118

GCGGGCTCCT TGACAATTTC TTCGTATCTG TTCTTGCCCC GC

42

2) INFORMATION FOR SEQ ID NO: 2119

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2119

GCGGGCTTAC AACCCTAAGG CTGTTCCATT CGTTGCCCGC

40

2) INFORMATION FOR SEQ ID NO: 2120

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

1091

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2120

GCGGGCAGAA ACCAAGGCTG GTAAGGTTAC CGGTAGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2121

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2121

CGACCGCIAG CCGCACACCA AGTTCGGTC G

31

2) INFORMATION FOR SEQ ID NO: 2122

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2122

CCGAGCGAAT GTAGGAGTCC AGGGTCTCTG CTCGG

35

2) INFORMATION FOR SEQ ID NO: 2123

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2123

TCTACCACTG AAGCATTAC

19

2) INFORMATION FOR SEQ ID NO: 2124

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2124

TAGGTACTGT AGGTTTATTG

20

2) INFORMATION FOR SEQ ID NO: 2125

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2125

CACGCGGATT TTGAATCTCT TCCTCTAGTA GCGCGTG

37

2) INFORMATION FOR SEQ ID NO: 2126

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2126

ATATCAGAGA CTGATGAG

18

2) INFORMATION FOR SEQ ID NO: 2127

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single

1093

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2127

TAGCATATTC AGAGAATATT GT

22

2) INFORMATION FOR SEQ ID NO: 2128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2128

CAACGCTGGA GAATCTATAT TTGTAGAAAC TCGGTTG

37

2) INFORMATION FOR SEQ ID NO: 2129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8133 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X51797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2129

ATGTCTTTAA	TATCTAAAGA	AGAGTTAATA	AAACTCGCAT	ATAGCATTAG	50
ACCAAGAGAA	AATGAGTATA	AAACTATACT	AACTAATTTA	GACGAATATA	100
ATAAGTTAAC	TACAAACAAT	AATGAAAATA	AATATTTGCA	ATTAAAAAAA	150
CTAAATGAAT	CAATTGATGT	TTTTATGAAT	AAATATAAAA	CTTCAAGCAG	200
AAATAGAGCA	CTCTCTAATC	TAAAAAAGA	TATATTAAAA	GAAGTAATTC	250
TTATTAAAAA	TTCCAATACA	AGCCCTGTAG	AAAAAAATTT	ACATTTTGTA	300
TGGATAGGTG	GAGAAGTCAG	TGATATTGCT	CTTGAATACA	TAAAACAATG	350
GGCTGATATT	AATGCAGAAT	ATAATATTAA	ACTGTGGTAT	GATAGTGAAG	400
CATTCTTAGT	AAATACACTA	AAAAAGGCTA	TAGTTGAATC	TTCTACCACT	450
GAAGCATTAC	AGCTACTAGA	GGAAGAGATT	CAAAATCCTC	AATTTGATAA	500
TATGAAATTT	TACAAAAAAA	GGATGGAATT	TATATATGAT	AGACAAAAAA	550
GGTTTATAAA	TTATTATAAA	TCTCAAATCA	ATAAACCTAC	AGTACCTACA	600
ATAGATGATA	TTATAAAGTC	TCATCTAGTA	TCTGAATATA	ATAGAGATGA	650
AACTGTATTA	GAATCATATA	GAACAAATTC	TTTGAGAAAA	ATAAATAGTA	700
ATCATGGGAT	AGATATCAGG	GCTAATAGTT	TGTTTACAGA	ACAAGAGTTA	750
TTAAATATTT	ATAGTCAGGA	GTTGTAAAT	CGTGGAAATT	TAGCTGCAGC	800

ATCTGACATA	GTAAGATTAT	TAGCCCTAAA	AAATTTTGGC	GGAGTATATT	850
TAGATGTTGA	TATGCTTCCA	GGTATTCAC	CTGATTTATT	TAAAACAATA	900
TCTAGACCTA	GCTCTATTGG	ACTAGACCGT	TGGGAAATGA	TAAAATTAGA	950
GGCTATTATG	AAGTATAAAA	AATATATAAA	TAATTATACA	TCAGAAAAC	1000
TTGATAAACT	TGATCAACAA	TTAAAAGATA	ATTTTAACT	CATTATAGAA	1050
AGTAAAAGTG	AAAAATCTGA	GATATTTTCT	AAATTAGAAA	ATTTAAATGT	1100
ATCTGATCTT	GAAATTAAAA	TAGCTTTCGC	TTTAGGCAGT	GTTATAAATC	1150
AAGCCTTGAT	ATCAAAACAA	GGTTCATATC	TTACTAACCT	AGTAATAGAA	1200
CAAGTAAAAA	ATAGATATCA	ATTTTAAAC	CAACACCTTA	ACCCAGCCAT	1250
AGAGTCTGAT	AATAACTTCA	CAGATACTAC	TAAAATTTTT	CATGATTCAT	1300
TATTTAATTC	AGCTACCGCA	GAAAACCTCTA	TGTTTTTAAC	AAAAATAGCA	1350
CCATACTTAC	AAGTAGGTTT	TATGCCAGAA	GCTCGCTCCA	CAATAAGTTT	1400
AAGTGGTCCA	GGAGCTTATG	CGTCAGCTTA	CTATGATTTT	ATAAATTTAC	1450
AAGAAAATAC	TATAGAAAAA	ACTTTAAAAG	CATCAGATTT	AATAGAATTT	1500
AAATTCCAG	AAAATAATCT	ATCTCAATTG	ACAGAACAAG	AAATAAATAG	1550
TCTATGGAGC	TTTGATCAAG	CAAGTGCAAA	ATATCAATTT	GAGAAATATG	1600
TAAGAGATTA	TACTGGTGGA	TCTCTTTCTG	AAGACAATGG	GGTAGACTTT	1650
AATAAAAATA	CTGCCCTCGA	CAAAAACCTAT	TTATTAAATA	ATAAAATTCC	1700
ATCAACAAT	GTAGAAGAAG	CTGGAAGTAA	AAATTATGTT	CATTATATCA	1750
TACAGTTACA	AGGAGATGAT	ATAAGTTATG	AAGCAACATG	CAATTTATTT	1800
TCTAAAAATC	CTAAAAATAG	TATTATTATA	CAACGAAATA	TGAATGAAAG	1850
TGCAAAAAGC	TACTTTTAA	GTGATGATGG	AGAATCTATT	TTAGAATTAA	1900
ATAAATATAG	GATACCTGAA	AGATTAAAAA	ATAAGGAAAA	AGTAAAAGTA	1950
ACCTTTATTG	GACATGGTAA	AGATGAATTC	AACACAAGCG	AATTTGCTAG	2000
ATTAAGTGTA	GATTCACCTT	CCAATGAGAT	AAGTTCATTT	TTAGATACCA	2050
TAAAATTAGA	TATATCACCT	AAAAATGTAG	AAGTAAACTT	ACTTGGATGT	2100
AATATGTTTA	GTTATGATTT	TAATGTTGAA	GAAACTTATC	CTGGGAAGTT	2150
GCTATTAAGT	ATTATGGACA	AAATTACTTC	CAGTTTACCT	GATGTAAATA	2200
AAAATTCTAT	TACTATAGGA	GCAAATCAAT	CATGAAGTAAG	AATTAATAGT	2250
GAGGGAAGAA	AAGAACTTCT	GGCTCACTCA	GGTAAATGGA	TAAATAAAGA	2300
AGAAGCTATT	ATGAGCGATT	TATCTAGTAA	AGAATACATT	TTTTTTGATT	2350
CTATAGATAA	TAAGCTAAAA	GCAAAGTCCA	AGAATATTCC	AGGATTAGCA	2400
TCAATACAG	AAGATATAAA	AACATTATTA	CTTGATGCAA	GTGTTAGTCC	2450
TGATACAAAA	TTTATTTTAA	ATAATCTTAA	GCTTAATATT	GAATCTTCTA	2500
TTGGGGATTA	CATTTATTAT	GAAAAATTAG	AGCCTGTAA	AAATATAATT	2550
CACAATTCTA	TAGATGATTT	AATAGATGAG	TTCAATCTAC	TTGAAAATGT	2600
ATCTGATGAA	TTATATGAAT	TAAAAAAATT	AAATAATCTA	GATGAGAAGT	2650
ATTTAATATC	TTTTGAAGAT	ATCTCAAAAA	ATAATTCAAC	TTACTCTGTA	2700
AGATTTATTA	ACAAAAGTAA	TGGTGAGTCA	GTTTATGTAG	AAACAGAAAA	2750
AGAAATTTTT	TCAAAATATA	GCGAACATAT	TACAAAAGAA	ATAAGTACTA	2800
TAAAGAATAG	TATAATTACA	GATGTTAATG	GTAATTTATT	GGATAATATA	2850
CAGTTAGATC	ATACTTCTCA	AGTTAATACA	TTAAACGCAG	CATTCTTTAT	2900
TCAATCATTA	ATAGATTATA	GTAGCAATAA	AGATGTACTG	AATGATTTAA	2950
GTACCTCAGT	TAAGGTTCAA	CTTTATGCTC	AACTATTTAG	TACAGGTTTA	3000
AATACTATAT	ATGACTCTAT	CCAATTAGTA	AATTTAATAT	CAAATGCAGT	3050
AAATGATACT	ATAAATGTAC	TACCTACAAT	AACAGAGGGG	ATACCTATTG	3100
TATCTACTAT	ATTAGACGGA	ATAAACTTAG	GTGCAGCAAT	TAAGGAATTA	3150
CTAGACGAAC	ATGACCCATT	ACTAAAAAAA	GAATTAGAAG	CTAAGGTGGG	3200
TGTTTTAGCA	ATAAATATGT	CATTATCTAT	AGCTGCAACT	GTAGCTTCAA	3250
TTGTTGGAAT	AGGTGCTGAA	GTTACTATTT	TCTTATTACC	TATAGCTGGT	3300
ATATCTGCAG	GAATACCTTC	ATTAGTTAAT	AATGAATTAA	TATTGCATGA	3350
TAAGGCAACT	TCAGTGGTAA	ACTATTTTAA	TCATTTGTCT	GAATCTAAAA	3400
AATATGGCCC	TCTTAAAACA	GAAGATGATA	AAATTTTAGT	TCCTATTGAT	3450
GATTTAGTAA	TATCAGAAAT	AGATTTTAA	AATAATTTCG	TAAAACCTAGG	3500
AACATGTAAT	ATATTAGCAA	TGGAGGGGGG	ATCAGGACAC	ACAGTGACTG	3550
GTAATATAGA	TCACCTTTTC	TCATCTCCAT	CTATAAGTTC	TCATATTCCCT	3600
TCATTATCAA	TTTATTCTGC	AATAGGTATA	GAAACAGAAA	ATCTAGATTT	3650

TTCAAAAAA	ATAATGATGT	TACCTAATGC	TCCTTCAAGA	GTGTTTTGGT	3700
GGGAAACTGG	AGCAGTTCCA	GGTTTAAGAT	CATTGGAAAA	TGACGGAAGT	3750
AGATTACTTG	ATTCAATAAG	AGATTTATAC	CCAGGTAAAT	TTTACTGGAG	3800
ATTCTATGCT	TTTTTCGATT	ATGCAATAAC	TACATTAAAA	CCAGTTTATG	3850
AAGACACTAA	TATTAAAATT	AAACTAGATA	AAGATACTAG	AAACTTCATA	3900
ATGCCAACTA	TAAGTACTAA	CGAAATTAGA	AACAAATTAT	CTTATTCATT	3950
TGATGGAGCA	GGAGGAACTT	ACTCTTTTAT	ATTATCTTCA	TATCCAATAT	4000
CAACGAATAT	AAATTTATCT	AAAGATGATT	TATGGATATT	TAATATTGAT	4050
AATGAAGTAA	GAGAAATATC	TATAGAAAAT	GGTACTATTA	AAAAAGGAAA	4100
GTTAATAAAA	GATGTTTTAA	GTAAAATTGA	TATAAATAAA	AATAAACTTA	4150
TTATAGGCAA	TCAAACAATA	GATTTTTTCAG	GCGATATAGA	TAATAAAGAT	4200
AGATATATAT	TCTTGACTTG	TGAGTTAGAT	GATAAAATTA	GTTTAATAAT	4250
AGAAATAAAT	CTTGTTGCAA	AATCTTATAG	TTTGTTATTG	TCTGGGGATA	4300
AAAATTATTT	GATATCCAAT	TTATCTAATA	CTATTGAGAA	AATCAATACT	4350
TTAGGCCTAG	ATAGTAAAAA	TATAGCGTAC	AATTACACTG	ATGAATCTAA	4400
TAATAAATAT	TTTGAGGCTA	TATCTAAAAC	AAGTCAAAAA	AGCATAATAC	4450
ATTATAAAAA	AGACAGTAAA	AATATATTAG	AATTTTATAA	TGACAGTACA	4500
TTAGAATTTA	ACAGTAAAGA	TTTTATTGCT	GAAGATATAA	ATGTATTTAT	4550
GAAAGATGAT	ATTAATACTA	TAACAGGAAA	ATACTATGTT	GATAATAATA	5000
CTGATAAAAG	TATAGATTTT	TCTATTTCTT	TAGTTAGTAA	AAATCAAGTA	5050
AAAGTAAATG	GATTATATTT	AAATGAATCC	GTATACTCAT	CTTACCTTGA	5100
TTTTGTGAAA	AATTCAGATG	GACACCATAA	TACTTCTAAT	TTTATGAATT	5150
TATTTTTTGA	CAATATAAGT	TTCTGGAAAT	TGTTTGGGTT	TGAAAATATA	5200
AATTTTGTA	TCGATAAATA	CTTTACCCTT	GTTGGTAAAA	CTAATCTTGG	5250
ATATGTAGAA	TTTATTTGTG	ACAATAATAA	AAATATAGAT	ATATATTTTG	5300
GTGAATGGAA	AACATCGTCA	TCTAAAAGCA	CTATATTTAG	CGGAAATGGT	5350
AGAAATGTTG	TAGTAGAGCC	TATATATAAT	CCTGATACGG	GTGAAGATAT	5400
ATCTACTTCA	CTAGATTTTT	CCTATGAACC	TCTCTATGGA	ATAGATAGAT	5450
ATATAAATAA	AGTATTGATA	GCACCTGATT	TATATACAAG	TTTAATAAAT	5500
ATTAATACCA	ATTATTATTC	AAATGAGTAC	TACCCTGAGA	TTATAGTTCT	5550
TAACCCAAAT	ACATTCCACA	AAAAAGTAAA	TATAAATTTA	GATAGTTCTT	5600
CTTTTGAGTA	TAAATGGTCT	ACAGAAGGAA	GTGACTTTAT	TTTAGTTAGA	5650
TACTTAGAAG	AAAGTAATAA	AAAAATATTA	CAAAAAATAA	GAATCAAAGG	5700
TATCTTATCT	AATACTCAAT	CATTTAATAA	AATGAGTATA	GATTTTAAAG	5750
ATATTAAAAA	ACTATCATT	GGATATATAA	TGAGTAATTT	TAAATCATT	5800
AATTCTGAAA	ATGAATTAGA	TAGAGATCAT	TTAGGATTTA	AAATAATAGA	5850
TAATAAAACT	TATTACTATG	ATGAAGATAG	TAAATTAGTT	AAAGGATTAA	5900
GCAAGTAATT	GACAATAATA	AGTATTATTT	CAATCCTGAC	ACTGCTATCA	5950
TCTCAAAAGG	TTGGCAGACT	GTTAATGGTA	GTAGATACTA	CTTTGATACT	6000
GATACCGCTA	TTGCCTTTAA	TGGTTATAAA	ACTATTGATG	GTAAACACTT	6050
TTATTTTGAT	AGTGATTGTG	TAGTGAAAAT	AGGTGTGTTT	AGTACCTCTA	6100
ATGGATTGTA	ATATTTTGCA	CCTGCTAATA	CTTATAATAA	TAACATAGAA	6150
GGTCAGGCTA	TAGTTTATCA	AAGTAAATTC	TTAACTTTGA	ATGGTAAAAA	6200
ATATTACTTT	GATAATAACT	CAAAAGCAGT	TACCGGATTG	CAAACATTATG	6250
ATAGTAAAAA	ATATTACTTT	AATACTAACA	CTGCTGAAGC	AGCTACTGGA	6300
TGGCAAACTA	TTGATGGTAA	AAAATATTAC	TTTAATACTA	ACACTGCTGA	6350
AGCAGCTACT	GGATGGCAAA	CTATTGATGG	TAAAAAATAT	TACTTTAATA	6400
CTAACACTGC	TATAGCTTCA	ACTGGTTATA	CAATTATTAA	TGGTAAACAT	6450
TTTTATTTTA	ATACTGATGG	TATTATGCAG	ATAGGAGTGT	TTAAAGGACC	6500
TAATGGATTT	GAATATTTTG	CACCTGCTAA	TACGGATGCT	AACAACATAG	6550
AAGGTCAAGC	TATACTTTAC	CAAAATGAAT	TCTTAACTTT	GAATGGTAAA	6600
AAATATTACT	TTGGTAGTGA	CTCAAAAGCA	GTTACTGGAT	GGAGAATTAT	6650
TAACAATAAG	AAATATTACT	TTAATCCTAA	TAATGCTATT	GCTGCAATTC	6700
ATCTATGCAC	TATAAATAAT	GACAAGTATT	ACTTTAGTTA	TGATGGAATT	6750
CTTCAAAATG	GATATATTAC	TATTGAAAGA	AATAATTTCT	ATTTTGATGC	6800
TAATAATGAA	TCTAAAATGG	TAACAGGAGT	ATTTAAAGGA	CCTAATGGAT	6850
TTGAGTATTT	TGCACCTGCT	AATACTCACA	ATAATAACAT	AGAAGGTCAG	6900

GCTATAGTTT	ACCAGAACAA	ATTCTTAACT	TTGAATGGCA	AAAAATATTA	6950
TTTTGATAAT	GACTCAAAAG	CAGTTACTGG	ATGGCAAACC	ATTGATGGTA	7000
AAAAATATTA	CTTTAATCTT	AACACTGCTG	AAGCAGCTAC	TGGATGGCAA	7050
ACTATTGATG	GTAAAAAATA	TTACTTTAAT	CTTAACACTG	CTGAAGCAGC	7100
TACTGGATGG	CAAACCTATTG	ATGGTAAAAA	ATATTACTTT	AATACTAACA	7150
CTTTCATAGC	CTCAACTGGT	TATACAAGTA	TTAATGGTAA	ACATTTTAT	7200
TTTAATACTG	ATGGTATTAT	GCAGATAGGA	GTGTTTAAAG	GACCTAATGG	7250
ATTTGAATAC	TTTGCACCTG	CTAATACGGA	TGCTAACAAAC	ATAGAAGGTC	7300
AAGCTATACT	TTACCAAAT	AAATTCTTAA	CTTTGAATGG	TAAAAAATAT	7350
TACTTTGGTA	GTGACTCAAA	AGCAGTTACC	GGACTGCGAA	CTATTGATGG	7400
TAAAAAATAT	TACTTTAATA	CTAACACTGC	TGTTGCAGTT	ACTGGATGGC	7450
AAACTATTAA	TGGTAAAAAA	TACTACTTTA	ATACTAACAC	TTCTATAGCT	7500
TCAACTGGTT	ATACAATTAT	TAGTGGTAAA	CATTTTATT	TTAATACTGA	7550
TGGTATTATG	CAGATAGGAG	TGTTTAAAGG	ACCTGATGGA	TTTGAATACT	7600
TTGCACCTGC	TAATACAGAT	GCTAACAAATA	TAGAAGGTCA	AGCTATACGT	7650
TATCAAAATA	GATTCCTATA	TTTACATGAC	AATATATATT	ATTTTGGTAA	7700
TAATTCAAAA	GCGGCTACTG	GTTGGGTAAAC	TATTGATGGT	AATAGATATT	7750
ACTTCGAGCC	TAATACAGCT	ATGGGTGCGA	ATGGTTATAA	AACTATTGAT	7800
AATAAAAATT	TTTACTTTAG	AAATGGTTTA	CCTCAGATAG	GAGTGTTTAA	7850
AGGGTCTAAT	GGATTTGAAT	ACTTTGCACC	TGCTAATACG	GATGCTAACA	7900
ATATAGAAGG	TCAAGCTATA	CGTTATCAAA	ATAGATTCCCT	ACATTTACTT	7950
GGAAAAATAT	ATTACTTTGG	TAATAATTCA	AAAGCAGTTA	CTGGATGGCA	8000
AACTATTAAT	GGTAAAGTAT	ATTACTTTAT	GCCTGATACT	GCTATGGCTG	8050
CAGCTGGTGG	ACTTTTCGAG	ATTGATGGTG	TTATATATTT	CTTGGTGTT	8100
GATGGAGTAA	AAGCCCCTGG	GATATATGGC	TAA		8133

2) INFORMATION FOR SEQ ID NO: 2130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X53138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2130

ATGAGTTT	TTAATAGAAA	ACAGTTAGAA	AAAATGGCAA	ATGTAAGATT	50
TCGTA	GAAGATGAAT	ATGTTGCAAT	ATTGGATGCT	TTAGAAGAAT	100
ATCATAATAT	GTCAGAGAAT	ACTGTAGTCG	AAAAATATTT	AAAAATTAAAA	150
GATATAAATA	GTTTAACAGA	TATTTATATA	GATACATATA	AAAAATCTGG	200
TAGAAATAAA	GCCTTAAAAA	AATTTAAGGA	ATATCTAGTT	ACAGAAGTAT	250
TAGAGCTAAA	GAATAATAAT	TTAACTCCAG	TTGAGAAAAA	TTTACATTTT	300
GTTTGGATTG	GAGGTCAAAT	AAATGACACT	GCTATTAATT	ATATAAATCA	350
ATGGAAAGAT	GTAAATAGTG	ATTATAATGT	TAATGTTTTT	TATGATAGTA	400
ATGCATTTTT	GATAAACACA	TTGAAAAAAA	CTGTAGTAGA	ATCAGCAATA	450
AATGATACAC	TTGAATCATT	TAGAGAAAAAC	TTAAATGACC	CTAGATTTGA	500
CTATAATAAA	TTCTTCAGAA	AACGTATGGA	AATAATTTAT	GATAAACAGA	550
AAAATTTTCAT	AAACTACTAT	AAAGCTCAAA	GAGAAGAAAA	TCCTGAACCTT	600

ATAATTGATG	ATATTGTAAA	GACATATCTT	TCAAATGAGT	ATTCAAAGGA	650
GATAGATGAA	CTTAATACCT	ATATTGAAGA	ATCCTTAAAT	AAAATTACAC	700
AGAATAGTGG	AAATGATGTT	AGAACTTTG	AAGAATTTAA	AAATGGAGAG	750
TCATTCAACT	TATATGAACA	AGAGTTGGTA	GAAAGGTGGA	ATTTAGCTGC	800
TGCTTCTGAC	ATATTAAGAA	TATCTGCATT	AAAAGAAATT	GGTGGTATGT	850
ATTTAGATGT	TGATATGTTA	CCAGGAATAC	AACCAGACTT	ATTTGAGTCT	900
ATAGAGAAAC	CTAGTTCAGT	AACAGTGGAT	TTTTGGGAAA	TGACAAAGTT	950
AGAAGCTATA	ATGAAATACA	AAGAATATAT	ACCAGAATAT	ACCTCAGAAC	1000
ATTTTGACAT	GTTAGACGAA	GAAGTTCAAA	GTAGTTTTGA	ATCTGTTCTA	1050
GCTTCTAAGT	CAGATAAATC	AGAAATATTC	TCATCACTTG	GTGATATGGA	1100
GGCATCACCA	CTAGAAGTTA	AAATTGCATT	TAATAGTAAG	GGTATTATAA	1150
ATCAAGGGCT	AATTTCTGTG	AAAGACTCAT	ATTGTAGCAA	TTTAATAGTA	1200
AAACAAATCG	AGAATAGATA	TAAAATATTG	AATAATAGTT	TAAATCCAGC	1250
TATTAGCGAG	GATAATGATT	TTAATACTAC	AACGAATACC	TTTATTGATA	1300
GTATAATGGC	TGAAGCTAAT	GCAGATAATG	GTAGATTTAT	GATGGAACTA	1350
GGAAAGTATT	TAAGAGTTGG	TTTCTTCCCA	GATGTTAAAA	CTACTATTAA	1400
CTTAAGTGGC	CCTGAAGCAT	ATGCGGCAGC	TTATCAAGAT	TTATTAATGT	1450
TTAAAGAAGG	CAGTATGAAT	ATCCATTTGA	TAGAAGCTGA	TTTAAGAAAC	1500
TTTGAAATCT	CTAAAACATA	TATTTCTCAA	TCAACTGAAC	AAGAAATGGC	1550
TAGCTTATGG	TCATTTGACG	ATGCAAGAGC	TAAAGCTCAA	TTTGAAGAAT	1600
ATAAAAGGAA	TTATTTTGAA	GGTCTCTTG	GTGAAGATGA	TAATCTTGAT	1650
TTTTCTCAAA	ATATAGTAGT	TGACAAGGAG	TATCTTTTAG	AAAAAATATC	1700
TTCATTAGCA	AGAAGTTCAG	AGAGAGGATA	TATACACTAT	ATTGTTTCAGT	1750
TACAAGGAGA	TAAAATTAGT	TATGAAGCAG	CATGTAACCT	ATTTGCAAAG	1800
ACTCCTTATG	ATAGTGTACT	GTTTCAGAAA	AATATAGAAG	ATTCAGAAAT	1850
TGCATATTAT	TATAATCCTG	GAGATGGTGA	AATACAAGAA	ATAGACAAGT	1900
ATAAAATTCC	AAGTATAATT	TCTGATAGAC	CTAAGATTAA	ATTAACATTT	1950
ATTGGTCATG	GTAAAGATGA	ATTTAATACT	GATATATTTG	CAGGTTTTGA	2000
TGTAGATTCA	TTATCCACAG	AAATAGAAGC	AGCAATAGAT	TTAGCTAAAG	2050
AGGATATTTT	TCCTAAGTCA	ATAGAAATAA	ATTTATTAGG	ATGTAATATG	2100
TTTAGCTACT	CTATCAACGT	AGAGGAGACT	TATCCTGGAA	AATTATTACT	2150
TAAAGTTAAA	GATAAAATAT	CAGAATTAAT	GCCATCTATA	AGTCAAGACT	2200
CTATTATAGT	AAGTGCAAAT	CAATATGAAG	TTAGAATAAA	TAGTGAAGGA	2250
AGAAGAGAA	TATTGGATCA	TTCTGGTGAA	TGGATAAATA	AAGAAGAAAG	2300
TATTATAAAG	GATATTTTCT	CAAAAGAATA	TATATCATT	AATCCTAAAG	2350
AAAATAAAAT	TACAGTAAAA	TCTAAAAATT	TACCTGAGCT	ATCTACATTA	2400
TTACAAGAAA	TTAGAAATAA	TTCTAATTCA	AGTGATATTG	AACTAGAAGA	2450
AAAAGTAATG	TTAACAGAAT	GTGAGATAAA	TGTTATTTCA	AATATAGATA	2500
CGCAAATTGT	TGAGGAAAGG	ATTGAAGAAG	CTAAGAATTT	AACTTCTGAC	2550
TCTATTAATT	ATATAAAAGA	TGAATTTAAA	CTAATAGAAT	CTATTTCTGA	2600
TGCACTATGT	GACTTAAAC	AACAGAATGA	ATTAGAAGAT	TCTCATTTTA	2650
TATCTTTTGA	GGACATATCA	GAGACTGATG	AGGGATTTAG	TATAAGATTT	2700
ATTAATAAAG	AAACTGGAGA	ATCTATATTT	GTAGAACTG	AAAAACAAT	2750
ATTCTCTGAA	TATGCTAATC	ATATACTGA	AGAGATTTCT	AAGATAAAAG	2800
GTACTATATT	TGATACTGTA	AATGGTAAGT	TAGTAAAAAA	AGTAAATTTA	2850
GATACTACAC	ACGAAGTAAA	TACTTTAAAT	GCTGCATTTT	TTATACAATC	2900
ATTAATAGAA	TATAATAGTT	CTAAAGAATC	TCTTAGTAAT	TTAAGTGTAG	2950
CAATGAAAGT	CCAAGTTTAC	GCTCAATTAT	TTAGTACTGG	TTTAAATACT	3000
ATTACAGATG	CAGCCAAAGT	TGTTGAATTA	GTATCAACTG	CATTAGATGA	3050
AACTATAGAC	TTACTTCCTA	CATTATCTGA	AGGATTACCT	ATAATTGCAA	3100
CTATTATAGA	TGGTGTAAGT	TTAGGTGCAG	CAATCAAAGA	GCTAAGTGAA	3150
ACGAGTGACC	CATTATTAAG	ACAAGAAATA	GAAGCTAAGA	TAGGTATAAT	3200
GGCAGTAAAT	TTAACAACAG	CTACAACGTC	AATCATTACT	TCATCTTTGG	3250
GGATAGCTAG	TGGATTTAGT	ATACTTTTAG	TTCTTTTAGC	AGGAATTTCA	3300
GCAGGTATAC	CAAGCTTAGT	AAACAATGAA	CTTGTAACCT	GAGATAAGGC	3350
AACAAAGGTT	GTAGATTATT	TTAAACATGT	TTCATTAGTT	GAAACTGAAG	3400
GAGTATTTAC	TTTATTAGAT	GATAAAATAA	TGATGCCACA	AGATGATTTA	3450

GTGATATCAG	AAATAGATTT	TAATAATAAT	TCAATAGTTT	TAGGTAAATG	3500
TGAAATCTGG	AGAATGGAAG	GTGGTTCAGG	TCATACTGTA	ACTGATGATA	3550
TAGATCACTT	CTTTTCAGCA	CCATCAATAA	CATATAGAGA	GCCACACTTA	3600
TCTATATATG	ACGTATTGGA	AGTACAAAAA	GAAGAACTTG	ATTTGTCAAA	3650
AGATTTAATG	GTATTACCTA	ATGCTCCAAA	TAGAGTATTT	GCTTGGGAAA	3700
CAGGATGGAC	ACCAGGTTTA	AGAAGCTTAG	AAAATGATGG	CACAAAACCTG	3750
TTAGACCGTA	TAAGAGATAA	CTATGAAGGT	GAGTTTTATT	GGAGATATTT	3800
TGCTTTTATA	GCTGATGCTT	TAATAACAAC	ATTAAAACCA	AGATATGAAG	3850
ATACTAATAT	AAGAATAAAT	TTAGATAGTA	ATACTAGAAG	TTTTATAGTT	3900
CCAATAATAA	CTACAGAATA	TATAAGAGAA	AAATTATCAT	ATTCCTTCTA	3950
TGGTTCAGGA	GGAACCTTATG	CATTGTCTCT	TTCTCAATAT	AATATGGGTA	4000
TAAATATAGA	ATTAAGTGAA	AGTGATGTTT	GGATTATAGA	TGTTGATAAT	4050
GTTGTGAGAG	ATGTAACCTAT	AGAATCTGAT	AAAATTAAAA	AAGGTGATTT	4100
AATAGAAGGT	ATTTTATCTA	CACTAAGTAT	TGAAGAGAAT	AAAATTATCT	4150
TAAATAGCCA	TGAGATTAAT	TTTTCTGGTG	AGGTAAATGG	AAGTAATGGA	4200
TTTGTTTCTT	TAACATTTTC	AATTTTAGAA	GGAATAAATG	CAATTATAGA	4250
AGTTGATTTA	TTATCTAAAT	CATATAAATT	ACTTATTTCT	GGCGAATTAA	4300
AAATATTGAT	GTTAAATTCA	AATCATATTC	AACAGAAAAT	AGATTATATA	4350
GGATTCAATA	GCGAATTACA	GAAAAATATA	CCATATAGCT	TTGTAGATAG	4400
TGAAGGAAAA	GAGAATGGTT	TTATTAATGG	TTCAACAAAA	GAAGGTTTAT	4450
TTGTATCTGA	ATTACCTGAT	GTAGTTCCTA	TAAGTAAGGT	TTATATGGAT	4500
GATAGTAAGC	CTTCATTTGG	ATATTATAGT	AATAATTTGA	AAGATGTCAA	4550
AGTTATAACT	AAAGATAATG	TTAATATATT	AACAGGTTAT	TATCTTAAGG	4600
ATGATATAAA	AATCTCTCTT	TCTTTGACTC	TACAAGATGA	AAAAACTATA	4650
AAGTTAAATA	GTGTGCATTT	AGATGAAAGT	GGAGTAGCTG	AGATTTTGAA	4700
GTTTCATGAAT	AGAAAAGGTA	ATACAAATAC	TTCAGATTCT	TTAATGAGCT	4750
TTTTAGAAAG	TATGAATATA	AAAAGTATTT	TCGTTAATTT	CTTACAATCT	4800
AATATTAAGT	TTATATTAGA	TGCTAATTTT	ATAATAAGTG	GTACTACTTC	4850
TATTGGCCAA	TTTGAGTTTA	TTTGTGATGA	AAATGATAAT	ATACAACCAT	4900
ATTTCAATTAA	GTTTAATACA	CTAGAAACTA	ATTATACTTT	ATATGTAGGA	4950
AATAGACAAA	ATATGATAGT	GGAACCAAAT	TATGATTTAG	ATGATTCTGG	5000
AGATATATCT	TCAACTGTTA	TCAATTTCTC	TCAAAAAGTAT	CTTTATGGAA	5050
TAGACAGTTG	TGTTAATAAA	GTTGTAATTT	CACCAAATAT	TTATACAGAT	5100
GAAATAAATA	TAACGCCTGT	ATATGAAACA	AATAATACTT	ATCCAGAAGT	5150
TATTGTATTA	GATGCAAATT	ATATAAATGA	AAAAATAAAT	GTTAATATCA	5200
ATGATCTATC	TATACGATAT	GTATGGAGTA	ATGATGGTAA	TGATTTTATT	5250
CTTATGTCAA	CTAGTGAAGA	AAATAAGGTG	TCACAAGTTA	AAATAAGATT	5300
CGTTAATGTT	TTTAAAGATA	AGACTTTGGC	AAATAAGCTA	TCTTTTAACT	5350
TTAGTGATAA	ACAAGATGTA	CCTGTAAGTG	AAATAATCTT	ATCATTTACA	5400
CCTTCATATT	ATGAGGATGG	ATTGATTGGC	TATGATTGGG	GTCTAGTTTC	5450
TTTATATAAT	GAGAAATTTT	ATATTAATAA	CTTTGGAATG	ATGGTATCTG	5500
GATTAATATA	TATTAATGAT	TCATTATATT	ATTTTAAACC	ACCAGTAAAT	5550
AATTTGATAA	CTGGATTTGT	GACTGTAGGC	GATGATAAAT	ACTACTTTAA	5600
TCCAATTAAT	GGTGGAGCTG	CTTCAATTGG	AGAGACAATA	ATTGATGACA	5650
AAAATTATTA	TTTCAACCAA	AGTGGAGTGT	TACAAACAGG	TGTATTTAGT	5700
ACAGAAGATG	GATTTAAATA	TTTTGCCCCA	GCTAATACAC	TTGATGAAAA	5750
CCTAGAAGGA	GAAGCAATTG	ATTTTACTGG	AAAATTAATT	ATTGACGAAA	5800
ATATTTATTA	TTTTGATGAT	AATTATAGAG	GAGCTGTAGA	ATGGAAAGAA	5850
TTAGATGGTG	AAATGCACTA	TTTTAGCCCA	GAAACAGGTA	AAGCTTTTAA	5900
AGGTCTAAAT	CAATAGGTG	ATTATAAATA	CTATTTCAAT	TCTGATGGAG	5950
TTATGCAAAA	AGGATTTGTT	AGTATAAATG	ATAATAACA	CTATTTTGAT	6000
GATTCTGGTG	TTATGAAAGT	AGGTTACACT	GAAATAGATG	GCAAGCATTT	6050
CTACTTTGCT	GAAAACGGAG	AAATGCAAAT	AGGAGTATTT	AATACAGAAG	6100
ATGGATTTAA	ATATTTTGCT	CATCATAATG	AAGATTTAGG	AAATGAAGAA	6150
GGTGAAGAAA	TCTCATATTC	TGGTATATTA	AATTTCAATA	ATAAAATTTA	6200
CTATTTTGAT	GATTCATTTA	CAGCTGTAGT	TGGATGGAAA	GATTTAGAGG	6250
ATGGTTCAAA	GTATTATTTT	GATGAAGATA	CAGCAGAAGC	ATATATAGGT	6300

TTGTCATTAA	TAAATGATGG	TCAATATTAT	TTTAATGATG	ATGGAATTAT	6350
GCAAGTTGGA	TTTGTCACTA	TAAATGATAA	AGTCTTCTAC	TTCTCTGACT	6400
CTGGAATTAT	AGAATCTGGA	GTACAAAACA	TAGATGACAA	TTATTTCTAT	6450
ATAGATGATA	ATGGTATAGT	TCAAATTGGT	GTATTTGATA	CTTCAGATGG	6500
ATATAAATAT	TTTGCACCTG	CTAATACTGT	AAATGATAAT	ATTTACGGAC	6550
AAGCAGTTGA	ATATAGTGGT	TTAGTTAGAG	TTGGGGAAGA	TGTATATTAT	6600
TTTGGAGAAA	CATATACAAT	TGAGACTGGA	TGGATATATG	ATATGGAAAA	6650
TGAAAGTGAT	AAATATTATT	TCAATCCAGA	AACTAAAAAA	GCATGCAAAG	6700
GTATTAATTT	AATTGATGAT	ATAAAATATT	ATTTTGATGA	GAAGGGCATA	6750
ATGAGAACGG	GTCTTATATC	ATTTGAAAAT	AATAATTATT	ACTTTAATGA	6800
GAATGGTGAA	ATGCAATTTG	GTTATATAAA	TATAGAAGAT	AAGATGTTCT	6850
ATTTTGGTGA	AGATGGTGTC	ATGCAGATTG	GAGTATTTAA	TACACCAGAT	6900
GGATTTAAAT	ACTTTGCACA	TCAAATACT	TTGGATGAGA	ATTTTGAGGG	6950
AGAATCAATA	AACTATACTG	GTTGGTTAGA	TTTAGATGAA	AAGAGATATT	7000
ATTTTACAGA	TGAATATATT	GCAGCAACTG	GTTTCAGTTAT	TATTGATGGT	7050
GAGGAGTATT	ATTTTGATCC	TGATACAGCT	CAATTAGTGA	TTAGTGAATA	7100
G					7101

2) INFORMATION FOR SEQ ID NO: 2131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2131

AAGCMATTGT TGTAATTTTT GAAAG

25

2) INFORMATION FOR SEQ ID NO: 2132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2132

TCATATCCAT AGCAATAGTT CTA

23

2) INFORMATION FOR SEQ ID NO: 2133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid

1100

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2133

CCACGCACAW AAACCTTGTTT TAGAAGTAGC AGCWCAGCGT GG

42

2) INFORMATION FOR SEQ ID NO: 2134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2134

CGCGTGAAGC TTCTGTG

17

2) INFORMATION FOR SEQ ID NO: 2135

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2135

TCTCGCCGTT ATTCAGTTTC

20

2) INFORMATION FOR SEQ ID NO: 2136

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2136

CCAACGCGTC CTCAATCATT TCTAACTTCT ATGGCCGGCG TTGG

44

2) INFORMATION FOR SEQ ID NO: 2137

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2137

ATGATCACCG	GTGCTGCCCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
CGCCGATGGT	CCGATGCCrC	AAACCCGTGA	GCACATCCTG	CTGTCCCGTC	100
AGGTAGGCGT	TCCGTACATC	GTGGTCTTCC	TGAACAAGGC	CGACCTGGTA	150
GACGACGCTG	AGCTGCTGGA	ACTGGTCGAG	ATGGAAGTTC	GCGACCTGCT	200
GTCCACCTAC	GACTTCCCAG	GCGACGACAC	TCCGATCATC	ATCGGTTCCG	250
CTCGTATGGC	CCTGGAAGGC	AAAGACGACA	ACGAAATGGG	CACTACCGCT	300
GTCAAGAAGC	TGGTAGAAAC	TCTGGATGCC	TACATCCCTG	AGCCAGTTCG	350
TGCCATCGAC	CAGCCGTTCC	TGATGCCGAT	CGAAGACGTG	TTCTCGATCT	400
CGGGTCGTGG	TACCGTTGTT	ACCGGTCGTA	TCGAGCGTGG	CATCGTTTCGC	450
GTTTCAGGATC	CGCTGGAAAT	CGTTGGTCTG	CGTGACACCA	CCACCACCAC	500
CTGCACCGGT	GTTGAGATGT	TCCGCAAGCT	GCTGGACGAA	GGTCGTGCTG	550
GCGAGAACTG	CGGCGTTCTG	CTGCGTG GTA	CCAAGCGTGA	CGACGTTGAG	600
CGTGGCCAGG	TTCTGGTCAA	GCCAGGTTTCG	GTCAAGCCGC	ACACCAAGTT	650
CACCGCAGAA	GTCTACGTCC	TGTCGAAGGA	AGAAGGCGGC	CGTCACACTC	700
CGTTCTTCAA	AGGCTACCGT	CCACAGTTCT	ACTTCCGTAC	CACTGACGTG	750
ACCGGTA ACT	GCGAACTGCC	GGAAGGCGTT	GAAATGGTAA	TGCCAGGTGA	800
CAACATTCAG	ATGACTGTTA	CCCTGATCAA	GACCATCGCA	ATGGAAGACG	850
GTCTGCGCTT	CGCTATCCGT	GAAGGCGGTC	GTACCGTCG		889

2) INFORMATION FOR SEQ ID NO: 2138

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*
- (B) STRAIN: PAO-1
- (C) ACCESSION NUMBER: Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2138

AACATGATCA	CCGGTGCTGC	CCAGATGGAC	GGCGCGATCC	TGGTTTGTCTC	50
GGCTGCCGAC	GGCCCCATGC	CGCAGACCCG	CGAGCACATC	CTGCTGTCCC	100
GCCAGGTAGG	CGTTCCCTAC	ATCGTCGTGT	TCCTGAACAA	GGCCGACATG	150
GTCGACGACG	CCGAGCTGCT	GGAAGTGGTC	GAGATGGAAG	TTGCGGATCT	200
GCTGAACACC	TACGACTTCC	CGGGCGACGA	CACTCCGATC	ATCATCGGTT	250
CCGCGCTGAT	GGCGCTGGAA	GGCAAGGATG	ACAACGGCAT	CGGCGTAAGC	300
GCCGTGCAGA	AGCTGGTAGA	GACCCTGGAC	TCCTACATTC	CGGAGCCGGT	350
TCGTGCCATC	GACCAGCCGT	TCCTGATGCC	GATCGAAGAC	GTGTTCTCGA	400
TCTCCGGCCG	CGGTACCGTG	GTAACCGGTC	GTGTAGAGCG	CGGCATCATC	450
AAGGTCCAGG	AAGAAGTGGA	AATCGTCGGC	ATCAAGGCGA	CCACCAAGAC	500
TACCTGCACC	GGCGTTGAAA	TGTTCCGCAA	GCTGCTCGAC	GAAGGTCGTG	550
CTGGTGAGAA	CGTTGGTATC	CTGCTGCGTG	GCACCAAGCG	TGAAGACGTA	600
GAGCGTGGCC	AGGTTCTGGC	CAAGCCGGGC	ACCATCAAGC	CGCACACCAA	650
GTTTCGAGTG	GAAGTGACG	TGCTGTCCAA	GGAAGAAGGT	GGTCGTCACA	700
CCCCGTTCTT	CAAGGGCTAC	CGTCCGCAGT	TCTACTTCCG	TACCACCGAC	750
GTGACCGGTA	ACTGCGAACT	GCCGGAAGGC	GTAGAGATGG	TAATGCCGGG	800
CGACAACATC	AAGATGGTTG	TCACCCTGAT	CGCTCCGATC	GCCATGGAAG	850
ATGGCCTGCG	CTTCGCGATC	CGCGAAGGCG	GCCGTACCGT	TGGCGCCGGC	900

2) INFORMATION FOR SEQ ID NO: 2139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni*
- (B) STRAIN: NCTC 11168
- (C) ACCESSION NUMBER: AL139074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2139

ATGCAAGGAT	TTATTTTACA	GGTATTAGGT	CCGGTTGTTG	ATGTAGATTT	50
TAACGACTAT	TTGCCTCAAA	TAAATGAAGC	AATTGTTGTA	AATTTTGAAA	100
GCGAAGGAAA	AAAACATAAA	CTTGTTTTAG	AAGTAGCAGC	TCATTTAGGA	150
GATAATAGAG	TTAGAACTAT	TGCTATGGAT	ATGACAGATG	GTTTGGTAAAG	200
GGGCTTAAAA	GCTGAGGCTT	TAGGTGCTCC	CATTAGTGTT	CCTGTTGGTG	250
AGAAAGTTTT	AGGAAGAATT	TTCAATGTTA	CTGGAGATTT	GATCGATGAA	300
GGTGAAGAAA	TTTCTTTCGA	TAAAAAATGG	GCAATTCATA	GAGATCCACC	350
AGCTTTTGAA	GATCAAAGCA	CAAAAAGTGA	GATTTTGTAA	ACAGGGATTA	400
AAGTTGTAGA	TTTACTTGCT	CCTTATGCAA	AAGGTGGTAA	AGTAGGTCTT	450
TTTGGTGGTG	CAGGTGTTGG	TAAAACTGTT	ATTATTATGG	AGCTTATTCA	500
CAATGTTGCA	TTTAAGCATA	GCGGCTATTC	TGTATTTGCA	GGTGTGGGTG	550
AGAGAACTCG	TGAAGGAAAT	GACCTTTATA	ATGAAATGAA	AGAAAGTAAT	600
GTTTTAGACA	AAGTTGCTCT	ATGTTATGGA	CAAATGAATG	AACCACCAGG	650
GGCAAGAAAT	CGTATTGCTT	TAACAGGTTT	AACAATGGCT	GAGTATTTTA	700
GAGATGAAAT	GGGTCTTGAT	GTGCTTATGT	TTATTGATAA	TATCTTTAGA	750
TTTTTACAAT	CAGGTTCTGA	AATGTCAGCA	CTTTTAGGAA	GAATTCCATC	800
AGCTGTGGGT	TATCAACCAA	CCTTAGCAAG	TGAAATGGGT	AAATTCCAAG	850
AAAGAATTAC	TTCAACTAAA	AAAGGCTCAA	TCACTTCAGT	TCAAGCTGTT	900
TACGTTCCAG	CTGATGACTT	AACAGACCCA	GCTCCAGCAA	CTGTTTTTGC	950

TCACTTAGAT	GCTACAACGG	TTTTAAATAG	AGCTATTGCT	GAAAAGGGTA	1000
TTTATCCTGC	AGTTGACCCA	CTTGACTCAA	CTTCAAGAAT	GCTTGACCCA	1050
AATATCATTG	GAGAAGAACA	TTATAAAGTT	GCTCGTGGTG	TTCAATCAGT	1100
GCTTCAAAAA	TACAAAGATT	TACAAGATAT	CATCGCCATT	TTAGGTATGG	1150
ATGAGCTTAG	CGAAGAGGAT	AAACTTGTAG	TTGAAAGAGC	AAGAAAGATT	1200
GAAAAATTCT	TATCACAACC	ATTTTTCGTT	GCAGAAGTTT	TCACAGGTAG	1250
CCCAGGAAAA	TATATAAGCC	TTGAAGATAC	AATAGCAGGA	TTTAAGGGAA	1300
TTTTAGAAGG	TAAATATGAT	CATTTACCAG	AAAATGCTTT	CTATATGGTT	1350
GGAAATATAG	ATGAAGCTAT	TGCAAAAGCG	GATAAATTAA	AAGGTTAA	1398

2) INFORMATION FOR SEQ ID NO: 2140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2157 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 670
- (C) ACCESSION NUMBER: X67867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2140

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTTTTTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATTG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTAA	GGCTCAGGAA	450
GCTTG GTTAG	CGATT CAGTT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCTGCT	TACATGGATA	ATTACCTCAA	GGAGGTCATC	AATCAAGTAG	850
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAAC TCCGA	950
TCAATACGTC	TCTTACCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACTTGAGGC	TCGTCAACCA	1050
GCAAGTAACG	TTTCATT TGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCGA	TTATGCACCT	GCCATAGAAT	1150
ACGGTGTTTA	TGATTCCACT	GCAACTATGG	TTAATGATAT	TCCTTATAAC	1200
TATCCGGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTTCCG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAC	CTTCCTTAAT	1350
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTTCAAG	1400

TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAATGG	1450
CTGCTGCTTA	TGCTGCCTTT	GCCAACGGTG	GAATTTACCA	CAAACCCATG	1500
TATATCAATA	AGGTCGTCTT	CAGTGACGGT	AGTAAAAAAG	AATTTTCAGA	1550
TGTAGGTACA	CGAGCTATGA	AAGAAACAAC	TGCTTACATG	ATGACCGAAA	1600
TGATGAAAAC	TGTCTTGGCA	TACGGAAC TG	GTCGTGGAGC	CTATCTCCCA	1650
TGGTTAGCGC	AAGCTGGTAA	GACAGGTACT	TCTAACTACA	CAGATGATGA	1700
AATTGAAAAA	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTCG	1800
AATCGTTTAA	CTCCTATCGT	TGGAGATGGT	TTCCTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAGAAACG	GGGAATTTGT	ATTCAAAAAT	1950
GGAGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAACAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCGATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
ACAACCA					2157

2) INFORMATION FOR SEQ ID NO: 2141

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2141

CACCAGTCAC AGAAAAGC

18

2) INFORMATION FOR SEQ ID NO: 2142

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2142

GCCTTAATTT CGGATAGTGC

20

2) INFORMATION FOR SEQ ID NO: 2143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1105

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2143

GAGAAAGAGC CCAATTATCT AATGT

25

2) INFORMATION FOR SEQ ID NO: 2144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3075 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: J2870
- (C) ACCESSION NUMBER: X75439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2144

TTGACAAAGA	AATATTTTAAA	CACCCAGAAT	GAAATATCAG	CATTTTGGAA	50
TACTCAAAAG	ATATTTTAAAA	AATCAATTGA	CAATAGAAAA	GGACAGGAAA	100
GTTTTGTTTT	TTATGACGGC	CCCCCACTG	CAAATGGCCT	TCCTCATGCT	150
GGCCATGTTT	TTGGAAGAGT	AATCAAGGAT	TTAGTTGCAA	GATTA AAAAC	200
TATGCAAGGT	TTTTATGTAG	AAAGAAAAGC	AGGATGGGAT	ACCCATGGCT	250
TACCA GTTGA	ATTAGAGGTT	GAAAAA AAAA	TTGGAATTAA	AGGAAAACAA	300
GACATTGAAA	AGTATGGAAT	AGAAAATTTT	ATAAATGAAT	GTAAAAAAAG	350
TGTATTTAAT	TATGAAAAAG	AATGGCGGGA	TTTTTCTAAA	GATTTAGGAT	400
ACTGGGTTGA	CATGGACTCC	CCCTATATAA	CTCTTGAGAA	TAATTATATT	450
GAAAGTGTAT	GGAATATATT	ATCTACATTC	CATAAAAAAG	GA CTATTATA	500
TAAGGGACAT	AAGGTGACTC	CTTATTGTAC	ACATGATCAA	ACCGCTTTAA	550
GTTCTCATGA	AGTAGCGCAA	GGCTATAAAA	ACGTTA AAGA	TTTATCAGCT	600
GTTGT TAAAT	TTCAACTTAC	AAATAGTAAA	GATACTTATT	TCTTAAGTTG	650
GACTACCACT	CCCTGGACTT	TGCCTGCAAA	TGTAGCATT A	GCTATAAATA	700
AAGATCTTAA	TTATTCAAAA	ATTCGGGTAG	AAAATGAGTA	TTATATCTTA	750
GCTACAGATC	TAATTAATTC	TATAATAACT	GAAAAATACG	AAATTAT TGA	800
TACCTTTTCA	GGAAGTAATT	TAATTAATTT	AAAATACATT	CCTCCTTTTG	850
AAAGCGACGG	TTTAGTTAAT	GCATATTACG	TTGTTGATGG	AGAATTTGTT	900
ACTAACTCAG	AAGGAACTGG	TATTGTTTCAT	ATAGCACCAG	CTCATGGGGA	950
AGATGACTAC	CAATTGGTTT	TAGAGCGTGA	TTTGGATTTC	TTAAATGTTA	1000
TAACAAGAGA	AGGAGTATAT	AATGATAGGT	TCCCTGAATT	AGTTGGTAAT	1050
AAAGCTAAAA	ATAGTGATAT	AGAAATCATA	AAATTATTAT	CCAAAAAACA	1100
ACTTTTATAT	AAAAAACAAA	AATATGAGCA	TAATTATCCT	CATTGTTGGA	1150
GATGTGGTAA	TCCTTTGATA	TATTATGCGA	TGGAAGGTTG	GTTTATTTAA	1200
ACA ACTAATT	TTAAGAATGA	AATTATTAAC	AATAATAATA	ATATAGAGTG	1250
GTTTCCTTCT	CATATTAAGG	AAGGGAGAAT	GGGAAATTTT	TTAGAAAATA	1300
TGGTTGATTG	GAACATTGGT	AGAAATAGAT	ATTGGGGAAC	ACCATTAAAT	1350
GTATGGATTT	GCAATGATTG	TAATCACGAA	TACGCACCAA	GTAGTATTAA	1400
GGATTTACAA	AATAATTCCA	TCAATAAAAT	TGATGAAGAT	ATTGAGTTGC	1450
ATAGACCTTA	TGTTGATAAT	ATCACTCTTA	GTTGCCCTAA	GTGTAATGGG	1500

1106

AAAATGTCTC	GAGTAGAAGA	AGTAATCGAT	GTTTGGTTTG	ATAGCGGCTC	1550
TATGCCGTTT	GCTCAGCATC	ATTATCCTTT	TGATAACCAG	AAAATTTTTA	1600
ATCAACACTT	TCCAGCTGAT	TTTATTGCAG	AAGGAGTTGA	TCAAACGAGA	1650
GGCTGGTTTT	ACAGTTTACT	AGTAATTTCT	ACTATTCTAA	AAGGAAAATC	1700
TTCTTATAAA	CGTGCTTTAT	CTTTAGGACA	TATTCTAGAC	AGTAATG GTA	1750
AAAAAATGTC	TAAAAGTAAA	GGAAACGTTA	TTAATCCAAC	TGAATTAATT	1800
AATAAGTACG	GAGCCGATTC	TTTAAGATGG	GCCTTAATTT	CGGATAGTGC	1850
TCCATGGAAT	AACAAAAGAT	TCTCAGAAAA	TATAGTAGCT	CAGACCAAAT	1900
CGAAATTTAT	AGATACGCTT	GATAATATTT	ATAAATTTTA	TAATATGTAT	1950
AATAAAATAG	ATCACTATAA	TCCTAATAAT	GAAATTACAA	AAAGTAGAAA	2000
TACATTAGAT	AATTGGGCTC	TTTCTCGCTT	AAACACCTTA	ATAAAAGAAA	2050
GTAATATTTA	TGTAAATAAT	TACGATTTCA	CTTCCGCAGC	CAGATTAATT	2100
AACGAATATA	CCAATACAAT	AAGTAATTGG	TATATCGGAG	ATTCGAGAGG	2150
ACGATTTTGG	GAACAAGGAA	TTTCTAACGA	TAAAAAAGAT	GCGTACAATA	2200
CGCTTTATGA	AATTTTAACA	ACTTTATCAA	GACTAGTGGC	TCCATTTGTT	2250
CCATTTATAT	CTGAAAAAAT	CCATTATAAT	TTGACTGGAA	AAAGTGTGCA	2300
TTTACAAGAT	TATCCACAAT	ATAAAGAAAG	TTTTATTAAT	CAAGCATTGG	2350
AAGATGAAAT	GCATACCGTT	ATAAAAATTG	TAGAATTATC	TAGACAGGCT	2400
CGCAAAAATG	CAGATTTAAA	AATTAAGCAA	CCTTTATCGA	AAATGGTGAT	2450
TAAACCTAAT	AGTCAATTAA	ACTTAAGTTT	TTTACCTAAT	TACTATTCAA	2500
TAATAAAAGA	CGAATTAAAT	ATAAAAAACA	TTGAATTAAC	TGATAATATT	2550
AATGACTATA	TTACCTATGA	GCTTAAATTG	AATTTTCTT	CTGTGGGACC	2600
AAAAC TAGGG	AACAAAACGA	AAAATATTCA	AACATTGATA	GACTCCCTAT	2650
CAGAGTATGA	TAAAAAAGT	TTAATTGAGT	CTAATAACTT	CAAAAGTTTA	2700
TCTTCTGATG	CTGAGTTAAC	TAAGGATGAT	TTTATAATTA	AAACCTTACC	2750
TAAGGATAGT	TATCAACTCA	GTGAAGATAA	TGACTGCGTT	ATATTATTAG	2800
ATAAAAATTT	ATCTCCTGAA	TTAATTCGCG	AAGGACATGC	TAGAGAGCTC	2850
ATTAGATTAA	TTCAACAATT	AAGAAAAAAG	AAAAATTTAC	CAATAAATCA	2900
ACGTATTGAT	ATTTATATCG	GTGTAAC TGG	GGAATTATTA	GAATCAATAA	2950
AAACCAATAA	AAATATGTTT	AAAGAAAATT	TCGTGATTAA	AAATATACAC	3000
TTAAATGTTA	TAGATGAATA	TGAAAATACT	ATTCATTTTA	ATAATAAAGA	3050
AATAAAAATT	TCCTTATTAT	ATTAA			3075

2) INFORMATION FOR SEQ ID NO: 2145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2145

GCAAGATGTG GCGTGTTACG GT

22

2) INFORMATION FOR SEQ ID NO: 2146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1107

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2146

GGGGCGAAGA AGTTGTCCAT ATT

23

2) INFORMATION FOR SEQ ID NO: 2147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (C) ACCESSION NUMBER: V00622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2147

ATGGAGAAAA	AAATCACTGG	ATATACCACC	GTTGATATAT	CCCAATGGCA	50
TCGTAAAGAA	CATTTTGAGG	CATTTTCAGTC	AGTTGCTCAA	TGTACCTATA	100
ACCAGACCGT	TCAGCTGGAT	ATTACGGCCT	TTTTAAAGAC	CGTAAAGAAA	150
AATAAGCACA	AGTTTTATCC	GGCCTTTATT	CACATTCTTG	CCCGCCTGAT	200
GAATGCTCAT	CCGGAATTCC	GTATGGCAAT	GAAAGACGGT	GAGCTGGTGA	250
TATGGGATAG	TGTTCAACCCT	TGTTACACCG	TTTTCCATGA	GCAAACCTGAA	300
ACGTTTTTCAT	CGTCTGGAG	TGAATACCAC	GACGATTTC	GGCAGTTTCT	350
ACACATATAT	TCGCAAGATG	TGGCGTGTTA	CGGTGAAAAC	CTGGCCTATT	400
TCCCTAAAGG	GTTTATTGAG	AATATGTTTT	TCGTCTCAGC	CAATCCCTGG	450
GTGAGTTTCA	CCAGTTTTGA	TTTAAACGTG	GCCAATATGG	ACAACTTCTT	500
CGCCCCCGTT	TTCACCATGG	GCAAATATTA	TACGCAAGGC	GACAAGGTGC	550
TGATGCCGCT	GGCGATTCAG	GTTTCATCATG	CCGTCTGTGA	TGGCTTCCAT	600
GTCGGCAGAA	TGCTTAATGA	ATTACAACAG	TACTGCGATG	AGTGGCAGGG	650
CGGGGCGTAA					660

2) INFORMATION FOR SEQ ID NO: 2148

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2148

CAGATTAAAT GCGGATTCAG CC

22

2) INFORMATION FOR SEQ ID NO: 2149

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2149

ATCAGGTAA TCATCAGCGG ATA

23

2) INFORMATION FOR SEQ ID NO: 2150

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 642 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*
 (B) STRAIN: K12
 (C) ACCESSION NUMBER: X53796
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2150

ATGAATTTTA	CCCGGATTGA	CCTGAATACC	TGGAATCGCA	GGGAACACTT	50
TGCCCTTTAT	CGTCAGCAGA	TTAAATGCGG	ATTCAGCCTG	ACCACCAAAC	100
TCGATATTAC	CGCTTTGCGT	ACCGCACTGG	CGGAGACAGG	TTATAAGTTT	150
TATCCGCTGA	TGATTTACCT	GATCTCCCGG	GCTGTTAATC	AGTTTCCGGA	200
GTTCCGGATG	GCACTGAAAG	ACAATGAACT	TATTTACTGG	GACCAGTCAG	250
ACCCGGTCTT	TACTGTCTTT	CATAAAGAAA	CCGAAACATT	CTCTGCACTG	300
TCCTGCCGTT	ATTTTCCGGA	TCTCAGTGAG	TTTATGGCAG	GTTATAATGC	350
GGTAACGGCA	GAATATCAGC	ATGATAACCAG	ATTGTTTCCG	CAGGGAAATT	400
TACCGGAGAA	TCACCTGAAT	ATATCATCAT	TACCGTGGGT	GAGTTTGTGAC	450
GGATTTAACC	TGAACATCAC	CGGAAATGAT	GATTATTTTG	CCCCGGTTTT	500
TACGATGGCA	AAGTTTCAGC	AGGAAGGTGA	CCGCGTATTA	TTACCTGTTT	550
CTGTACAGGT	TCATCATGCA	GTATGTGATG	GCTTTCATGC	AGCACGGTTT	600
ATTAATACAC	TTCAGCTGAT	GTGTGATAAC	ATACTGAAAT	AA	642

2) INFORMATION FOR SEQ ID NO: 2151

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 bases
 (B) TYPE: Nucleic acid

1109

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2151

ATATTTCAGC ATTACCTTGG GTT

23

2) INFORMATION FOR SEQ ID NO: 2152

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2152

TACACAACCTC TTGTAGCCGA TTA

23

2) INFORMATION FOR SEQ ID NO: 2153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Shigella flexneri*
(C) ACCESSION NUMBER: X07848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2153

ATGAACTATA	CAAAATTTGA	TGTAAAAAAT	TGGGTTTCGCC	GTGAGCATTT	50
TGAGTTTTAT	CGGCATCGTT	TACCATGTGG	TTTTAGCTTA	ACAAGCAAAA	100
TTGATATCAC	GACGTTAAAA	AAGTCATTGG	ATGATTCAGC	GTATAAGTTT	150
TATCCGGTAA	TGATCTATCT	GATTGCTCAG	GCCGTGAATC	AATTTGATGA	200
GTTGAGAATG	GCGATAAAAG	ATGATGAATT	GATCGTATGG	GATTCAGTCG	250
ACCCACAATT	CACCGTATTC	CATCAAGAAA	CAGAGACATT	TTCAGCACTG	300
AGTTGCCCAT	ACTCATCCGA	TATTGATCAA	TTTATGGTGA	ATTATTTATC	350
GGTAATGGAA	CGTTATAAAA	GTGATACCAA	GTTATTTCTT	CAAGGGGTAA	400
CACCAGAAAA	TCATTTAAAT	ATTTTCAGCAT	TACCTTGGGT	TAATTTTGAT	450
AGCTTTAATT	TAAATGTTGC	TAATTTTACC	GATTATTTTG	CACCCATTAT	500
AACAATGGCA	AAATATCAGC	AAGAAGGGGA	TAGACTGTTA	TTGCCGCTCT	550
CAGTACAGGT	TCATCATGCA	GTTTGTGATG	GCTTCCATGT	TGCACGCTTT	600
ATTAATCGGC	TACAAGAGTT	GTGTAACAGT	AAATTAAAAT	AA	642

2) INFORMATION FOR SEQ ID NO: 2154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2154

CGCCATTCAG AGTTTAGGAC

20

2) INFORMATION FOR SEQ ID NO: 2155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2155

TTCCATACCG TTGCGTATCA CTT

23

2) INFORMATION FOR SEQ ID NO: 2156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
- (B) STRAIN: CP590
- (C) ACCESSION NUMBER: M74769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2156

ATGGTATTTG	AAAAAATTGA	TAAAAATAGT	TGGAACAGAA	AAGAGTATTT	50
TGACCACTAC	TTTGCAAGTG	TACCTTGATC	ATACAGCATG	ACCGTTAAAG	100
TGGATATCAC	ACAAATAAAG	GAAAAGGGAA	TGAAACTATA	TCCTGCAATG	150
CTTTATTATA	TTGCAATGAT	TGTAAACCGC	CATTCAGAGT	TTAGGACGGC	200
AATCAATCAA	GATGGTGAAT	TGGGGATATA	TGATGAGATG	ATACCAAGCT	250

1111

ATACAATATT	TCACAATGAT	ACTGAAACAT	TTTCCAGCCT	TTGGACTGAG	300
TGTAAGTCTG	ACTTTAAATC	ATTTT TAGCA	GATTATGAAA	GTGATACGCA	350
ACGGTATGGA	AACAATCATA	GAATGGAAGG	AAAGCCAAAT	GCTCCGGA	400
ACATTTTAA	TGTATCTATG	ATACCGTGGT	CAACCTTCGA	TGGCTTTAAT	450
CTGAATTTGC	AGAAAGGATA	TGATTATTTG	ATTCTTATT	TTACTATGGG	500
GAAATATTAT	AAAGAAGATA	ACAAAATTAT	ACTTCCTTTG	GCAATTCAAG	550
TTCATCACGC	AGTATGTGAC	GGATTTTACA	TTTGCCGTTT	TGTAAACGAA	600
TTGCAGGAAT	TGATAAATAG	TTAA			624

2) INFORMATION FOR SEQ ID NO: 2157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2157

CCACAGAAAT TGATATTAGT GTTTTAT

27

2) INFORMATION FOR SEQ ID NO: 2158

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2158

TCGCTATTGT AACCAGTTCT A

21

2) INFORMATION FOR SEQ ID NO: 2159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: V01277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2159

ATGAACTTTA	ATAAAATTGA	TTTAGACAAT	TGGAAGAGAA	AAGAGATATT	50
TAATCATTAT	TTGAACCAAC	AAACGACTTT	TAGTATAACC	ACAGAAATTG	100
ATATTAGTGT	TTTATACCGA	AACATAAAAC	AAGAAGGATA	TAAATTTTAC	150
CCTGCATTTA	TTTTCTTAGT	GACAAGGGTG	ATAAACTCAA	ATACAGCTTT	200
TAGAACTGGT	TACAATAGCG	ACGGAGAGTT	AGGTATTATTGG	GATAAGTTAG	250
AGCCACTTTA	TACAATTTTT	GATGGTGTAT	CTAAAACATT	CTCTGGTATT	300
TGGACTCCTG	TAAAGAATGA	CTTCAAAGAG	TTTTATGATT	TATACCTTTC	350
TGATGTAGAG	AAATATAATG	GTTTCGGGGAA	ATTGTTTCCC	AAAACACCTA	400
TACCTGAAAA	TGCTTTTTCT	CTTTCTATTA	TTCCATGGAC	TTCATTTACT	450
GGGTTTAACT	TAAATATCAA	TAATAATAGT	AATTACCTTC	TACCCATTAT	500
TACAGCAGGA	AAATTCATTA	ATAAAGGTAA	TTCAATATAT	TTACCGCTAT	550
CTTTACAGGT	ACATCATTCT	GTTTGTGATG	GTTATCATGC	AGGATTGTTT	600
ATGAACTCTA	TTCAGGAATT	GTCAGATAGG	CCTAATGACT	GGCTTTTATA	650
A					651

2) INFORMATION FOR SEQ ID NO: 2160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2160

TTTTGAACAC TATTTTAACC AGC

23

2) INFORMATION FOR SEQ ID NO: 2161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2161

GATTTAACTT ATCCCAATAA CCT

23

2) INFORMATION FOR SEQ ID NO: 2162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

1113

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(C) ACCESSION NUMBER: X02166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2162

ATGACTTTTA	ATATTATCAA	ATTAGAAAAT	TGGGATAGAA	AAGAATATTT	50
TGAACACTAT	TTTAACCAGC	AAACTACGTA	TAGCATTACT	AAAGAAATTG	100
ATATTACTTT	GTTTAAAGAT	ATGATAAAAA	AGAAAGGATA	TGAAATTTAT	150
CCTTCTTTGA	TTTATGCAAT	TATGGAAGTT	GTAAATAAAA	ATAAAGTGTT	200
TAGAACAGGA	ATTAATAGTG	AGAATAAAAT	AGGTTATTGG	GATAAGTTAA	250
ATCCTTTTGT	TACAGTTTTT	AATAAGCAAA	CTGAAAAATT	TACTAACATT	300
TGGACTGAAT	CTGATAACAA	CTTCACTTCT	TTTTATAATA	ATTATAAAAA	350
TGACTTGCTT	GAATATAAAG	ATAAAGAAGA	AATGTTTCCT	AAAAAACCGA	400
TACCTGAAAA	CACCATACCG	ATTTCAATGA	TTCCTTGGAT	TGATTTTAGT	450
TCATTTAATT	TAAACATTGG	TAACAATAGC	AACTTTTTAT	TGCCTATTAT	500
TACGATAGGT	AAATTTTATA	GTGAGAATAA	TAAAATTTAT	ATACCAGTTG	550
CTTTGCAGCT	TCATCATGCT	GTATGTGATG	GTTACCATGC	TTCATTATTT	600
ATGAATGAAT	TTCAAGATAT	AATTCATAAG	GTAGATGATT	GGATTTAG	648

2) INFORMATION FOR SEQ ID NO: 2163

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2163

ACCTTCATCC TACCGATGTG GGTT

24

2) INFORMATION FOR SEQ ID NO: 2164

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2164

CAACGACACC AGCACTGCCA TTG

23

2) INFORMATION FOR SEQ ID NO: 2165

1114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
- (B) STRAIN: H3380
- (C) ACCESSION NUMBER: AF071555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2165

ATGACCACCA	CACGCCCCGC	GTGGGCCTAT	ACGCTGCCGG	CAGCACTGCT	50
GCTGATGGCT	CCTTTCGACA	TCCTCGCTTC	ACTGGCGATG	GATATTTATC	100
TCCCTGTCGT	TCCAGCGATG	CCCGGCATCC	TGAACACGAC	GCCCGCTATG	150
ATCCAACCTCA	CGTTGAGCCT	CTATATGGTG	ATGCTCGGCG	TGGGCCAAGT	200
GATTTTTTGGT	CCGCTCTCAG	ACAGAATCGG	GCGACGGCCA	ATTCTACTTG	250
CGGGCGCAAC	GGCTTTCGTC	ATTGCGTCTC	TGGGAGCAGC	TTGGTCTTCA	300
ACTGCACCGG	CCTTTGTGCG	TTTCCGTCTA	CTTCAAGCAG	TGGGCGCGTC	350
GGCCATGCTG	GTGGCGACGT	TCGCGACGGT	TCGCGACGTT	TATGCCAACC	400
GTCCTGAGGG	TGTCGTCATC	TACGGCCTTT	TCAGTTCGAT	GCTGGCGTTC	450
GTGCCTGCGC	TCGGCCCTAT	CGCCGGAGCA	TTGATCGGCG	AGTTCTTGGG	500
ATGGCAGGCG	ATATTCATTA	CTTTGGCTAT	ACTGGCGATG	CTCGCACTCC	550
TAAATGCGGG	TTTCAGGTGG	CACGAAACCC	GCCCTCTGGA	TCAAGTCAAG	600
ACGCGCCGAT	CTGTCTTGCC	GATCTTCGCG	AGTCCGGCTT	TTTGGGTTTA	650
CACTGTCCGC	TTTAGCGCCG	GTATGGGCAC	CTTCTTCGTC	TTCTTCTCGA	700
CGGCTCCCCG	TGTGCTCATA	GGCCAAGCGG	AATATTCCGA	GATCGGATTC	750
AGCTTTGCCT	TCGCCACTGT	CGCGCTTGTA	ATGATCGTGA	CAACCCGTTT	800
CGCGAAGTCC	TTTGTGCTCA	GATGGGGCAT	CGCAGGATGC	GTGGCGCGTG	850
GGATGGCGTT	GCTTGTTTGC	GGAGCGGTCC	TGTTGGGGAT	CGGCGAACTT	900
TACGGCTCGC	CGTCATTCTT	CACCTTCATC	CTACCGATGT	GGGTTGTCTG	950
GGTCGGTATT	GTCTTCACGG	TGTCCGTTAC	CGCGAACGGC	GCTTTGGCAG	1000
AGTTTCGACGA	CATCGCGGGA	TCAGCGGTCTG	CGTTCTACTT	CTGCATCCAA	1050
AGCCTGATAG	TCAGTATCGT	CGGGACATTG	GCGGTGACGC	TGTTAAACGG	1100
CGATACAGCG	TGGCCCGTGA	TTTGTTACGC	CACGGCAATG	GCAGTGCTGG	1150
TGTCGTTGGG	GCTGGCGCTC	CTTCGATCCC	GTGATGCTGC	CACCGAGAAG	1200
TCGCCAGTCG	TCTAG				1215

2) INFORMATION FOR SEQ ID NO: 2166

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2166

GACAAACCAT TCCTGCTG

1115

2) INFORMATION FOR SEQ ID NO: 2167

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2167

CAGCAGCTGG GCGGCGGT

18

2) INFORMATION FOR SEQ ID NO: 2168

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2168

CATCAAAGTT GGTGAAGAAG TTG

23

2) INFORMATION FOR SEQ ID NO: 2169

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2169

CCCGTTTGCG AAAGGTGG

18

2) INFORMATION FOR SEQ ID NO: 2170

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single

1116

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2170

ACGTGACGTT GACAAACCA

19

2) INFORMATION FOR SEQ ID NO: 2171

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2171

TCGTTGGATT AACTGAAGAA

20

2) INFORMATION FOR SEQ ID NO: 2172

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2172

GTGTTGAAAT GTTCCGTAAA

20

2) INFORMATION FOR SEQ ID NO: 2173

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2173

AAGAAAAAAT CTTCGAACTG GCTA

24

2) INFORMATION FOR SEQ ID NO: 2174
1117

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2174

TCTACACGGC CGGTG

15

2) INFORMATION FOR SEQ ID NO: 2175

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2175

CCGCCATACC CCGTTT

16

2) INFORMATION FOR SEQ ID NO: 2176

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2176

CGGCATTACC ATTTCCACAC CTTT

24

2) INFORMATION FOR SEQ ID NO: 2177

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2177

GGCACGGACA AACCATTCTT GCTGCCTATC GAAGACGTGT TCCCGTGCC

49

2) INFORMATION FOR SEQ ID NO: 2178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2178

GGCACGACAA ACCATTCTTG CTGCCTATCG AACGTGCC

38

2) INFORMATION FOR SEQ ID NO: 2179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2179

GGCAGCTCTA CTTCCGTACC ACTGACGTAA CCGGCTGCC

39

2) INFORMATION FOR SEQ ID NO: 2180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2180

TTCGCCGGCG TGGGC

15

2) INFORMATION FOR SEQ ID NO: 2181

(i) SEQUENCE CHARACTERISTICS:

1119

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2181

AGCGCCACGC GCAGG

15

2) INFORMATION FOR SEQ ID NO: 2182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2182

GCGCGCCAAC GACTTCTACC ACGAAATGGA AGAGTCGCGC GC

42

2) INFORMATION FOR SEQ ID NO: 2183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*
- (B) STRAIN: ATCC 8750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2183

TATCTTGGTT	WGCTCGGCCG	CTGACGGCCC	AATGCCTCAG	ACTCGCGAGC	50
ACATCCTGCT	GAGCCGTCAG	GTTGGCGTTC	CTTACATCAT	CGTGTTCTTG	100
AACAAGGCCG	ACATGGTTGA	TGACGAAGAG	CTGATCGAAC	TGGTTGAAAT	150
GGAAGTTCGC	GAGCTGTTGT	CCAAGTACGA	CTTCCCTGGC	GACGACACCC	200
CGATCATCAA	GGGTTTCGCC	AAACTGGCTC	TGGAAGGCGA	CGAAGGCCCA	250
CTGGGCAGCC	AAGCCGTTCT	GGCTCTGGCC	GAAGCGCTGG	ACAACCTACAT	300
TCCTACGCCT	GAGCGTGCCG	TTGACGGTAC	GTTCCCTGATG	CCTGTTGAAG	350
ACGTGTTCTC	GATCTCCGGC	CGTGGTACGG	TTGTGACCGG	TCGTATTGAG	400
CGCGGCATCA	TCAAGGTCGG	CGAAGAAATC	GAAATCGTGG	GTATCAAAGA	450
CACGGTCAAG	ACCATTTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACCAGGGCGA	AGCTGGCGAT	AACGTCGGTC	TGCTGCTGCG	TGGTACCAAG	550
CGTGAAGACG	TGGAACGTGG	TCAAGTTCTG	GCCAAGCCAG	GCTCGATCAA	600
GCCACACACT	GAATTTCGACG	CCGAGGTGTA	CATTCTGTCC	AAAGAAGAAG	650
GTGGTCGTCA	CACTCCTTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700

1120

CGTACAAC	CTG	CGA	AG	ACA	AGG	AAAT	750
GGTTCTG	CCA	GGCGA	CAACA	TTTCG	ATGAA	AGTGTCCCTG	800
TCGCCAT	GGA	AGAAG	GT				817

2) INFORMATION FOR SEQ ID NO: 2184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter coli*
- (B) STRAIN: ATCC 43479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2184

TACAATTGAA	GTTGAAAGAT	CTATGCGTGT	TCTTGATGGT	GCTGTTGCGG	50
TATTTTGTTT	AGTGGGTGGG	GTGCAGCCTC	AAAGTGAAAC	AGTTTGGAGA	100
CAAGCAAATA	AATATGGTGT	TCCAAGAATA	GTATTTGTAA	ATAAAATGGA	150
TAGAATCGGT	GCAAATTTCT	ACAATGTAGA	AGATCAAATT	CGCAACCGTT	200
TAAAAGCTAA	TCCAGTTCCA	CTTCAAATTC	CAATCGGTGC	TGAGGATAAT	250
TTTAAAGGCG	TAATCGATCT	TGTAACATG	AAAGCTTTAG	TTTGGAAGA	300
TGATACTAAG	CCAACGGATT	ATGTAGAAAA	AGAAATTCCA	GCTGAACTTA	350
AAGAAAAGGC	AGAAGAATAT	CGCACAAAAA	TGATAGAAGC	AGTTTCTGAA	400
ACTTCAGATG	AGTTGATGGA	AAAATATTTA	GGTGGAGAAG	AATTAAGCCT	450
TGAAGAGATT	AAAACAGGGA	TTAAAGCAGG	ATGTTTAAGT	CTTTCTATCG	500
TTCCATATGCT	TTGCGGTACA	GCGTTTAAAA	ATAAAGGGGT	TCAACCTTTG	550
CCTGATGCTG	TTGTGGCTTA	TTTACCAGCT	CCTGATGAAG	TTGCTAATAT	600
CAAAGGGGAA	TATGAAGACG	GCACAGAAGT	TTCTGTAAAA	TCAACTGATG	650
ATGGCGAATT	TGCAGGACTT	GCATTTAAAA	TTATGACAGA	TCCATTTGTA	700
GGACAACTTA	CTTTCGTGCG	TGTTTATCGT	GGATGTTTAG	AAAGCGGTTC	750
TTATGCTTAT	AACTCAACCA	AAGATAAAAA	AGAAAGAATT	GGTCGTTTGT	800
TAAAAATGCA	CTCTAATAAA	AGAGAAGAAA	TTAAAGTTCT	TTACGCAGGA	850
GAAATCGGTG	CAGTTGTAGG	ACTTAAAGAT	ACTTTAACAG	GGGATACTCT	900
TGCAAGTGAA	AAAGATAAAG	TAATTCTTGA	AAGAATGGAT	TTCCCAGACC	950
CAGTTATTTT	TGTTGCAGTA	GAMCCAAAAA	CTAAAGCAGA	TCAAGAAAAA	1000
ATGTCTATTG	CACTAAATAA	ATTAGCTCAA	GAAGATCCAA	GCTTTAGAGT	1050
TTCTACGGAT	GAAGAAAGTG	GTCAAACAT	CATTTCAAGT	ATGGGTGAAT	1100
TACACCTTGA	AATTATTGTT	GATCGTATGC	TTCGTGAATT	TAAAGTGGA	1150
GCTGAAGTGG	GACAACCTCA	AGTTGCTTAT	CGTGAAACTA	TCAGAAAAAC	1200
TGTTGAGCAA	GAATACAAAT	ACGCTAAGCA	ATCAGGCGGT	CGTGGTCAGT	1250
ATGGACATGT	ATTCTTACGC	CTTGAGCCAC	TTGAGCCAGG	AAGTGGATAC	1300
GAGTTTGTTA	ACGACATCAA	AGGTGGGGTA	ATTCCAAAAG	AATATATTCC	1350
TGCAGTAGAT	AAGGGTGTTC	AAGAAGCATT	GCAAAATGGT	GTTTTAGCAG	1400
GTTATCCAGT	AGAAGATGTT	AAAGTAACTG	TTTATGATGG	AAGTTATCAC	1450
GAGGTGGATT	CATCTGAGAT	GGCATTTAAA	CTTGCTGCTT	CTATGGGATT	1500
TAAAGAGGGT	GCTAGAAAAG	CAGGTGCTGT	GATCTTAGAG	CCTATGATGA	1550
AAGTTGAAGT	AGAAACTCCT	GAAGATTACA	TGGGCGATGT	TATTGGCGAT	1600
CTTAATAAGC	GTCGTGGTCA	AGTAAATAGC	ATGGATGAAA	GAGGTGGTAA	1650
TA					1652

2) INFORMATION FOR SEQ ID NO: 2185

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
- (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2185

GCTATTCTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AGACCCGTGA	50
GCACATCCTA	TTAGCACGTC	AGGTAGGCGT	ACCATACATC	ATCGTATTCC	100
TAAACAAGTG	CGATATGGTT	GACGACGAGG	AATTATTAGA	GTTAGTTGAG	150
ATGGACGTAC	GTGATCTATT	AAATCAGTAC	CAGTTCCCAG	GCGACGACAC	200
TCCAATCATC	CGTGGTTCAG	CACTAGGTGC	ATTAAACGGC	GAAGAGAAGT	250
GGAAAGAGGC	AATCTATCAG	TTAGCAGACA	CTCTAGATTC	ATACATTCCA	300
GAGCCAAAGC	GTGATATCGA	TGATCCATTC	CTATTACCAA	TCGAAGATAT	350
CTTCTCAATC	TCAGGTCGTG	GTACTGTAGT	AACCGGCCGT	GTAGAGCGTG	400
GTATTGTACA	CGTAGGTGAC	GAAGTTGAAA	TCGTTGGTAT	TCGTCCAACC	450
ACCAAGACCA	CTGTAAGTGG	CGTTGAAATG	TTCCGTAAGT	TACTAGACGA	500
AGGTCGTGCA	GGTGATAACG	TTGGTGTTCT	ACTACGTGGT	ACCAAGCGTG	550
ATGAGGTTGA	GCGTGGTCAG	GTTCTAGCTG	CTCCAGGCAC	AATCACTCCA	600
CACACCAAGT	TCACTGGTCA	GGTTTACGTA	CTAAGCAAGG	ATGAAGGTGG	650
TCGTCACACT	CCATTCTTCA	AGGGCTACCG	TCCACAGTTC	TTCTTCCGTA	700
CAACCGATAT	TACCGGTTCT	ATCGATCTGA	AAGAGGGCGT	AGAGATGGTA	750
ATGCCAGGTG	ATAACACCGA	CATGACCGTA	ACCCTAATCC	ACCCAGTAGC	800
TATGGCTGAA	GGCGAGAGAT				820

2) INFORMATION FOR SEQ ID NO: 2186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2186

ACGCGCTCAA AGCAGAAGTA TACGTATTAT CAAAAGACGC GCGT

44

2) INFORMATION FOR SEQ ID NO: 2187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1612 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2187

CAGTGGGTGG	GGTGCAGCCT	CAAAGTGAAA	CAGTTTGGAG	ACAAGCAAAT	50
AAATATGGTG	TTCCAAGAAT	AGTATTTGTA	AACAAAATGG	ATAGAATCGG	100
TGCAAAATTC	TACAATGTAG	AAGATCAAAT	TCGCAACCGT	TTAAAAGCTA	150
ATCCAGTTCC	ACTTCAAAT	CCAATCGGTG	CTGAGGATAA	TTTTAAAGGC	200
GTAATCGATC	TTGTAACAT	GAAAGCTTTA	GTTTGGGAAG	ATGATACTAA	250
GCCAACGGAT	TATGTAGAAA	AAGAAATTC	AGCTGAACTT	AAAGAAAAGG	300
CAGAAGAATA	TCGCACAAAA	ATGATAGAAG	CAGTTTCTGA	AACTTCAGAT	350
GAGTTGATGG	AAAAATATTT	AGGCGGAGAA	GAATTAAGCC	TTGAAGAGAT	400
TAAAACAGGG	ATTAAAGCAG	GATGTTTAAG	TCTTTCTATC	GTTCCCTATG	450
TTTGCGGTAC	AGCGTTTAAA	AATAAAGGGG	TTCAACCTTT	ACTTGATGCT	500
GTTGTGGCTT	ATTTACCAGC	TCCTGATGAA	GTGGCAAATA	TCAAGGGTGA	550
ATATGAAGAT	GGCACAGAAG	TTTCTGTAAA	ATCAACTGAT	GATGGCGAGT	600
TTGCAGGACT	TGCATTTAAA	ATTATGACAG	ATCCATTTGT	AGGACAACCT	650
ACTTTCGTGC	GTGTTTATCG	CGGTTGTTTA	GAAAGTGGTT	CTTATGCTTA	700
TAACTCAACT	AAAGATAAAA	AAGAAAGAAT	TGGTCGTTTG	TTAAAAATGC	750
ACTCTAACCA	AAGAGAAGAG	ATTAAAGTGC	TTTACGCAGG	CGAAATTGGT	800
GCTGTTGTAG	GACTTAAAGA	TACTTTAACA	GGGGATACTC	TTGTAAGTGA	850
AAAAGATAAG	GTAATCCTTG	AAAGAATGGA	TTTTCCAGAT	CCAGTTATTT	900
CTGTTGCAGT	TGAGCCAAAA	ACTAAAGCAG	ATCAAGAAAA	AATGTCTATT	950
GCTTTTAAATA	AATTAGCACA	AGAAGATCCA	AGTTTTAGAG	TTTCTACAGA	1000
TGAAGAAAGT	GGCCAAACTA	TCATTTTCAGG	TATGGGTGAG	TTACACCTTG	1050
AAATTATCGT	TGATAGAATG	CTTCGTGAAT	TTAAAGTTGA	AGCTGAAGTA	1100
GGTCAACCAC	AAGTTGCTTA	TCGCGAAACT	ATTAGAAAAA	CTGTTGAACA	1150
AGAATACAAA	TACGCTAAAC	AATCAGGTGG	TCGTGGTCAG	TATGGACATG	1200
TATTCTTACG	CCTTGAACCA	CTTGAGCCAG	GTAGTGGATA	TGAATTTGTT	1250
AATGATATCA	AAGGTGGAGT	AATTCCAAAA	GAATACATTC	CTGCAGTTGA	1300
TAAAGGTGTT	CAAGAAGCAT	TACAAAATGG	TGTTTTAGCA	GGTTATCCTG	1350
TGGAAGATGT	TAAAGTAACT	GTTTATGATG	GAAGTTATCA	CGAGGTGGAT	1400
TCATCTGAGA	TGGCGTTTAA	ACTTGCTGCT	TCTATGGGCT	TTAAAGAAGG	1450
TGCTAGAAAA	GCAGGTGCTG	TGATCTTAGA	GCCTATGATG	AAAGTTGAAG	1500
TAGAAACTCC	TGAAGATTAC	ATGGGTGATG	TTATTGGAGA	TCTTAACAAA	1550
CGCCGTGGTC	AAGTAAATAG	CATGGATGAG	CGTGGTGGA	ATAAAATCAT	1600
CACAGCATTT	TG				1612

2) INFORMATION FOR SEQ ID NO: 2188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
 (B) STRAIN: ATCC 33560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2188

ACAATTGAAG	TTGAAAGATC	TATGCGTGTT	CTTGATGGTG	CTGTTGCGGT	50
ATTTTGTTC	GTGGGTGGG	TGCAGCCTCA	AAGTGAAACA	GTTTGGAGAC	100
AAGCAAATA	ATATGGTGTT	CCAAGAATAG	TATTTGTAAA	TAAAATGGAT	150
AGAATCGGT	CAAATTTCTA	CAATGTAGAA	GATCAAATTC	GCAACCGTTT	200
AAAAGCTAAT	CCAGTTCAC	TTCAAATTC	AATTGGTGCT	GAGGATAATT	250
TTAAAGGCGT	AATCGATCTT	GTAACATGA	AAGCTTTAGT	TTGGGAAGAT	300
GATACTAAGC	CAACGGATTA	TGTAGAAAA	GAAATTCCAG	CTGAACCTAA	350
AGAAAAGGCA	GAAGAATATC	GCACAAAAAT	GATAGAAGCA	GTTTCTGAAA	400
CTTCAGATGA	GTTGATGGAA	AAATATTTAG	GCGGAGAAGA	ATTAAGCCTT	450
GAAGAGATTA	AAACAGGGAT	TAAAGCAGGA	TGTTTAAGTC	TTTCTATCGT	500
TCCTATGCTT	TGCGGTACAG	CGTTTAAAA	TAAAGGGGTT	CAACCTTTGC	550
TTGATGCTGT	TGTGGCTTAT	TTACCAGCTC	CTGATGAAGT	GGCAAATATC	600
AAGGGTGAAT	ATGAAGATGG	CACAGAAGTT	TCTGTAAAA	CAACTGATGA	650
TGGCGAGTTT	GCAGGACTTG	CATTTAAAA	CATGACAGAT	CCATTTGTAG	700
GACAACTTAC	TTTCGTGCGT	GTTTATCGCG	GTTGTTTAGA	AAGCGGTTCT	750
TATGCGTATA	ACTCAACTAA	AGATAAAAA	GAAAGAATTG	GTCGTTTGTT	800
AAAAATGCAC	TCTAACAAAA	GAGAAGAGAT	TAAAGTGCTT	TACGCAGGCG	850
AAATTGGTGC	TGTTGTAGGA	CTTAAAGATA	CTTTAACAGG	GGATACTCTT	900
GCAAGTGAAA	AAGATAAGGT	AATCCTTGAA	AGAATGGATT	TTCCAGATCC	950
AGTTATTTCT	GTTGCAGTTG	AGCCAAAAAC	TAAAGCTGAT	CAAGAAAAAA	1000
TGTCTATTGC	TTTAAATAAA	TTAGCACAA	AAGATCCAAG	TTTTAGAGTT	1050
TCTACAGATG	AAGAAAGTGG	TCAAACATATC	ATTTCAAGTA	TGGGTGAGTT	1100
ACACCTTGAA	ATTATCGTTG	ATAGAATGCT	TCGTGAATTT	AAAGTTGAAG	1150
CTGAAGTAGG	TCAACCACAA	GTTGCTTATC	GCGAAACTAT	TAGAAAAACT	1200
GTTGAACAAG	AATACAAATA	CGCTAAACAA	TCAGGTGGTC	GTGGTCAGTA	1250
TGGACATGTA	TTCTTACGCC	TTGAACCACT	TGAGCCAGGT	AGTGGATATG	1300
AATTTGTAA	TGATATCAA	GGTGGGGTAA	TTCCAAAAGA	ATACATTCTT	1350
GCAGTTGATA	AAGGTGTTCA	AGAAGCATTA	CAAATGGTG	TTTTAGCAGG	1400
TTATCCTGTG	GAAGATGTTA	AAGTAACTGT	TTATGATGGA	AGTTATCACG	1450
AGGTGGATTC	ATCTGAGATG	GCGTTTAAAC	TTGCTGCTTC	TATGGGCTTT	1500
AAAGAAGGTG	CTAGAAAAGC	AGGCGCTGTG	ATCTTAGAGC	CTATGATGAA	1550
AGTTGAAGTA	GAAACTCCTG	AAGATTATAT	GGGTGATGTT	ATTGGAGATC	1600
TTAACAAACG	CCGTGGTCAA	GTAAATAGCA	TGGATGAGCG	TGGTGGAAT	1650
AAAATCATCA	CAGCATT				1667

2) INFORMATION FOR SEQ ID NO: 2189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1255 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania guyanensis*
 (B) STRAIN: ATCC 50126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2189

TGACGGCGCT	GGACGTGACG	GAGGACCTCG	GCCGCGATGA	GCCGCTGACG	50
CTGGAGATCG	TGCAGCACTT	GGATGCGAAC	ACCGGCCGCT	GCATTGCGAT	100
GCAGACGACG	GACCTGCTGA	AGCTGAAGTC	GAAGGTTGTG	TCGACCGGCG	150
GCAACATCTC	CGTGCCGGTG	GGCCGCGAGA	CACTGGGCCG	CATCTTCAAC	200
GTGCTGGGCG	ACGCGATTGA	CCACCGCGGC	CCCCTGTGCG	AGAAGATGCG	250
CATGGCGATC	CACGCCGAGG	CGCCGAAGCT	GGCGGACCAG	GCTGCGGAGG	300
ACACGATCCT	GACGACCGGC	ATCAAGGTGA	TCGACCTGAT	TCTGCCCTAC	350
TGCAAGGGCG	GCAAGATCGG	CCTGTTCCGC	GGTGCCGGTG	TGGGCAAGAC	400
TGTGATCATC	ATGGAGCTGA	TCAACAACGT	CGCGAAGGGG	CACGGCGGCT	450
TCTCCGTGTT	CGCCGGCGTT	GGCGAGCGCA	CGCGCGAGGG	CACGGACCTG	500
TACCTGGAGA	TGATGCAGTC	AAAGGTGATT	GACCTGAAGG	GCGAGTCGAA	550
GTGCGTGCTT	GTGTACGGGC	AGATGAACGA	GCCCCCGGGT	GCGCGCGCGC	600
GCGTTGCGCA	GTCTGCGCTG	ACGATGGCCG	AGTACTTCCG	CGACGTGGAG	650
GGCCAGAACG	TGCTGCTGTT	CATCGACAAC	ATCTTCCGCT	TCACGCAGGC	700
GAACTCCGAG	GTGTCTGCGC	TGCTGGGCCG	CATCCCGGCC	GCCGTGGGTT	750
ACCAGCCGAC	GCTTGCGGAG	GATCTTGGCA	TGCTGCAGGA	GCGCATTACG	800
TCGACGACGA	AGGGATCGAT	TACGTCTGTG	CAGGCTGTGT	ACGTGCCTGC	850
GGATGATATC	ACGGACCCCG	CGCCCGCGAC	GACGTTCTCG	CACCTGGACG	900
CGACGACTGT	GCTGGACCGC	GCGGTGGCCG	AGTCGGGCAT	CTACCCTGCC	950
GTGAACCCGC	TGGAGTGCGC	GTCGCGCATC	ATGGACCCCG	ATGTGATCGA	1000
CGTGGACCAT	TACAACGTTG	CACAGGATAT	CGTCCAGATG	CTGACCAAGT	1050
ACAAGGAGCT	GCAGGACATC	ATTGCCGTGC	TTGGCATCGA	CGAGCTGAGC	1100
GAGGAGGACA	AGGTCGTGGT	GGACCGCGCG	CGCAAGGTGA	CGCGGTTTCT	1150
GTCGCAGCCG	TTCCAGGTTG	CGAGGTTGTT	CACCGGCATG	ACGGGCCACT	1200
ACGTGCAGCT	GAGCGACACG	GTGGAGTCGT	TCTCTGGCCT	GCTGATGGGG	1250
TCGTA					1255

2) INFORMATION FOR SEQ ID NO: 2190

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1248 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*
 (B) STRAIN: EATRO 795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2190

GCCCTTGACG	TTGTTGACAA	ACTTGGCCGT	GATGAGCCTC	TTACTCTTGA	50
GATCGTGACG	CATCTTGACG	CCCACACGGG	CCGCTGTATC	GCGATGCAAA	100
CGACGGATCT	CCTCAAACCTG	AAGGCAAAGG	TCGTTTTCGAC	AGGTGGCAAC	150
ATTTCCGTTT	CTGTCGGCCG	GGAAACACTA	GGTCGTATCT	TCAACGTGCT	200
TGGAGACGCT	ATTGACCAGC	GCGGCCCCGT	TGGTGAGAAA	CTGCGCATGC	250
CCATCCATGC	CGTGGCTCCC	AAGCTTGCGG	ACCAGGCCGC	TGAGGATGCG	300
GTGCTCACAA	CTGGTATTAA	GGTGATTGAT	CTCATTCTCC	CTTACTGCAA	350

AGGTGGA AAAA	ATTGGCCTCT	TTGGGGGTGC	GGGTGTGGGC	AAAACCGTCA	400
TTATTATGGA	GCTCATTAAC	AACGTTGCCA	AGGGTCACGG	TGGTTTCTCT	450
GTCTTCGCTG	GTGTTGGTGA	GCGTACCCGT	GAGGGAACGG	ATTTGTATCT	500
TGAGATGATG	CAGTCTAAGG	TTATTGACCT	TAAGGGTGAG	TCCAAATGTG	550
TGTTGGTGTA	CGGTCAGATG	AACGAGCCCC	CAGGTGCCCG	TGCGCGTGTT	600
GCGCAGTCGG	CTCTGACGAT	GGCTGAGTAC	TTCCGTGATG	TGGAGGGCCA	650
AGATGTGCTT	CTTTTTATCG	ACAATATTTT	TCGTTTCACT	CAGGCTAACT	700
CCGAGGTGTC	GGCGCTTCTG	GGTCGTATTG	CCGCCGCTGT	TGGCTACCAG	750
CCTACCCTCG	CTGAGGATCT	AGGGCAGTTG	CAGGAGCGTA	TTACCTCAAC	800
AACGAAAGGC	TCCATTACTT	CTGTGCAGGC	CGTATACGTG	CCGGCCGATG	850
ACATTACCGA	TCCAGCTCCA	GCAACAACCT	TCTCACATCT	GGACGCCACA	900
ACTGTGTTGG	ACCGTGCTGT	TGCCGAGTCT	GGTATCTACC	CCGCTGTTAA	950
CCCACTGGAA	TGCGCCTCGC	GTATCATGGA	CCCCGACGTT	ATCAGTGTGG	1000
ATCACTACAA	TGTTGCACAA	GATGTGGTAC	AGATGCTCAC	CAAGTACAGG	1050
GAATTACAGG	ATATCATTGC	TGTCCTTGGT	ATCGACGAGC	TAAGCGAGGA	1100
GGACAAACTT	ATCGTGGACC	GTGCGCGTAA	GTTGGTGAAG	TTCTCTCCC	1150
AGCCATTCCA	AGTTGCTGAG	GTCTTCACAG	GAATGACTGG	CCATTACGTG	1200
CAGTTGGATG	ACACCATCGA	TTCCTTTTCT	GGTCTCCTCA	TGGGTACG	1248

2) INFORMATION FOR SEQ ID NO: 2191

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
- (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2191

GAGCTGATTG	TAAGTCATCG	ACCACTTGAT	ATATGAATAC	ATCTAACAGT	50
AGTAGAACAA	CATCGCCAAG	GCTCACGGTG	GTTACTCCGT	CTTCACTGGT	100
GTCGGTGAGC	GTACTCGTGA	GGGTAACGAT	CTGTACCACG	AAATGCAGGA	150
GACTGGTGTC	ATTCAGCTCG	ACGGCGAATC	CAAGGTGTCT	CTTGTGTTTCG	200
GTCAGATGAA	CGAGCCCCCA	GGTGCTCGTG	CCCGTGTCGC	CCTTACTGGT	250
CTGACCATCG	CCGAATACTT	CCGTGACGAG	GAGGGTCAGG	ACGTGCTGCT	300
CTTCATTGAC	AACATTTTCC	GTTTCACCCA	GGCCGGTTCC	GAGGTGTCTG	350
CCCTTCTTGG	TCGTATCCCC	TCTGCCGTCG	GTTACCAGCC	CACTCTGGCC	400
GTCGACATGG	GTGGTATGCA	GGAACGTATT	ACCACCACCA		440

2) INFORMATION FOR SEQ ID NO: 2192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1262 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania panamensis*

(B) STRAIN: ATCC 50158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2192

GCTGACGGCG	CTGGACGTGA	CGGAGGACCT	CGGCCGCGAT	GAGCCGCTGA	50
CGCTGGAGAT	CGTGACGAC	TTGGATGCGA	ACACCGGCCG	CTGCATTGCG	100
ATGCAGACGA	CGGACCTGCT	GAAGCTGAAG	TCGAAGGTTG	TGTCGACCCG	150
CGGCAACATC	TCCGTGCCCG	TGGGCCGCGA	GACGCTGGGC	CGCATCTTCA	200
ACGTGCTGGG	CGACGCGATT	GACCACCGCG	GCCCCGTGTG	CGAGAAGATG	250
CGCATGGCGA	TCCACGCCGA	GGCGCCGAAG	CTGGCGGACC	AGGCTGCGGA	300
GGACACGATC	CTGACGACCG	GCATCAAGGT	GATCGACCTG	ATTCTGCCCT	350
ACTGCAAGGG	CGGCAAGATC	GGCCTGTTCG	GCGGTGCCCG	TGTGGGCAAG	400
ACTGTGATCA	TCATGGAGCT	GATCAACAAC	GTCGCGAAGG	GGCACGGCGG	450
CTTCTCCGTG	TTCGCCGGCG	TTGGCGAGCG	CACGCGCGAG	GGCACGGACC	500
TGTACCTGGA	GATGATGCAG	TCAAAGGTGA	TTGACCTGAA	GGGCGAGTCG	550
AAGTGCGTGC	TTGTGTACGG	GCAGATGAAC	GAGCCCCCGG	GTGCGCGCGC	600
GCGCGTTGCG	CAGTCTGCGC	TGACGATGGC	CGAGTACTTC	CGCGACGTGG	650
AGGGCCAGAA	CGTGCTGCTG	TTCATCGACA	ACATCTTCCG	CTTCACGCAG	700
GCGAACTCCG	AGGTGTCTGC	GCTGCTGGGC	CGCATCCCGG	CCGCCGTGGG	750
TTACCAGCCG	ACGCTTGCGG	AGGATCTTGG	CATGCTGCAG	GAGCGCATTA	800
CGTCGACGAC	GAAGGGATCG	ATTACGTCTG	TGCAGGCTGT	GTACGTGCCT	850
GCGGATGATA	TCACGGACCC	CGCGCCCGCG	ACGACGTTCT	CGCACCTGGA	900
CGCGACGACT	GTGCTGGACC	GCGCGGTGGC	GGAGTCGGGC	ATCTACCCTG	950
CCGTGAACCC	GCTGGAGTGC	GCGTCGCGCA	TCATGGACCC	CGATGTGATC	1000
GACGTGGACC	ATTACAACGT	TGCACAGGAT	ATCGTCCAGA	TGCTGACCAA	1050
GTACAAGGAG	CTGCAGGACA	TCATTGCGGT	GCTTGGCATC	GACGAGCTGA	1100
GCGAGGAGGA	CAAGGTCGTG	GTGGACCGCG	CGCGCAAGGT	GACGCGGTTC	1150
CTGTGCGCAG	CGTTCCAGGT	TGCGGAGGTG	TTCACCGGCA	TGACGGGCCA	1200
CTACGTGCAG	CTGAGCGACA	CGGTGGAGTC	GTTCTCTGGC	CTGCTGATGG	1250
GGTCGTACGA	CC				1262

2) INFORMATION FOR SEQ ID NO: 2193

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 912 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus nidulans*

(B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2193

TTCCGATGGT	CAAATGTACG	ATTGATATTC	CTTCCAGCCA	GTCAGGATAA	50
CAGCTGATAC	CAGTTGCAAA	TAGGCCCCAG	ACTCGTGAGC	ACTTGTGCT	100
TGCCCCTCAG	GTTGGTGTCC	AGAAGATCGT	TGTCTTCGTC	AACAAGGTTG	150
ACGCTGTCTGA	TGACCTTGAG	ATGTTGGAGC	TTGTTGAGCT	CGAGATGCGT	200

GAGCTCCTCA	ACACTTACGG	TTTCGAGGGA	GAGGAGACCC	CTATCATCTT	250
CGGTTCCGCC	CTGTGCGCTC	TCGAAGGCCG	CCGCGAGGAC	ATTGGTACTC	300
AGCGTATTGA	CTCCCTCCTC	GAGGCCGTTG	ACACTTGGAT	CCCTACCCCC	350
CAGCGTGA CT	TGGACAAGCC	CTTCCTGATG	TCCATTGAGG	AAGTTTTCTC	400
CATTGGTGGT	CGTGGTACCG	TCGCCTCTGG	TCGTGTCGAG	CGTGGTCTCC	450
TCAAGAAGGA	TACCGAAGTT	GAAATTCACG	GTGCTGATGG	TATTCTGAAG	500
ACCAAGGTCA	CCGACATTGA	GACCTTCAAG	AAGAGCTGCG	ATGAGTCTCG	550
TGCTGGTGAC	AACTCCGGTC	TTCTCCTCCG	TGGTATCCGT	CGTGAGGATG	600
TTCGTCGTGG	TATGGTCATC	GCTGCCCTG	GCTCCATCAA	GGCCTCCAAG	650
AAGTTCATGG	TCTCCATGTA	CGTCTTGACT	GAGGCTGAAG	GTGGCCGCAA	700
GAACGGCTTC	GGTGCCA ACT	ACCGCCCCCA	GGCTTTTCATC	CGCACTGCTG	750
GTAAGTTTCG	AACTATTTGA	TTCATTGATC	ACGTCCCTAA	CTGTTACTTT	800
AGACGAGGCT	TGCGACCTTC	ATTTCCCTGA	TGAGGCCGAC	AAGGACCGCC	850
ACGTCATGCC	CGGTGACAAC	GTCGAAATGG	TCCTCAACCT	CAACAACCCC	900
GTTGCTGCTG	AG				912

2) INFORMATION FOR SEQ ID NO: 2194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 887 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
- (B) STRAIN: WSA-234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2194

TCATCGTCGT	CGCCGCTTCT	GACGGTCAGA	TGCCCCAGAC	CAGAGAGCAC	50
TTGCTTCTCG	CCCGTCAGGT	CGGTATCCAG	AAGATTGTCT	TCTTCGTCAA	100
CAAGGTCGAC	GCCATCGAGG	ACAAGGAGAT	GCTTGAGCTC	GTCGAGATGG	150
AGATGCGTGA	GCTCCTCAGC	AGCTACGGCT	TCGAGGGTGA	CGAGACCCCC	200
ATCGTCATGG	GTTCCGCTCT	TTGTGCCCTT	GAGAACCGCC	AGCCCGAGAT	250
TGGAACCACC	CAGATCGACA	ACCTGATGAA	CGCTGTCGAC	GAGTGGATCC	300
CCACTCCCCA	GAGAGATCTT	GAGAAGCCCT	TCCTCATGTC	CGTTGAGGAT	350
GTCTTCTCTA	TCCCCGGTCG	TGGTACTGTC	GTTTCTGGCC	GTGTTGAGCG	400
TGGTACCCTG	AAGAAGGATT	CCGAAATCGA	GCTTGTCGGC	AAGAACAAGG	450
TCCCCATCAA	GACCAAGGTC	ACCGACATCG	AGACCTTCAA	GAAGTCTTGC	500
GACGAGTCCC	GCGCTGGTGA	CAACTCCGGT	CTTCTGCTCC	GTGGTATCAA	550
GCGTGAGGAT	GTCAACCGTG	GTATGGTTGT	CGTCAAGCCC	GGTACCGTCA	600
CCTCGCACAA	GAAGTTCCTC	GTCTCCATGT	ACGTCCTGAC	CAAGGAGGAG	650
GGTGGTTCGT	ACACTGGTTT	CCACGGAAAC	TACCGTCCCC	AGATCTTCAT	700
CCGTACCGCT	GGTAAGTCCT	GACTTTGAAC	TGCTGACCAA	TTTTCGCATC	750
TCTAACATGT	TTTACAGACG	AGGCTGCCGC	TATTGACTGG	CCCGAAGGCA	800
CCGAGGACGC	TGACTCCAAG	ATGGTCATGC	CCGGTGACAA	CGTCGAGATG	850
GTCTGCTCTC	TTCACAGACC	TCTTGCCGTT	GAACAGG		887

2) INFORMATION FOR SEQ ID NO: 2195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
- (B) STRAIN: ATCC 10784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2195

TGACGGCCAA	ATGTAGGACT	CTTGCGCGGG	ACTGACTGAT	TGGGGGGAAT	50
CCATTTTTTC	TTTTTCTTT	TTCTTTTTGA	GTACATGATT	ATACTAATAT	100
TTGGATAACG	TACCAGGCCT	CAAACACGTG	AACATTTACT	CCTTGCCCGA	150
CAAGTCGGTG	TCCAGAAGAT	CGTCGTTTTC	GTAAACAAGG	TCGATGTTCT	200
CGAAGATAAG	GAGATGTTGG	AGCTTGTCGA	GTTGGAAATG	AGAGAGCTCT	250
TGAACACCTA	CGGATTCGAG	GGTGAGGAAA	CGCCCATCAT	CTTCGGTTCT	300
GCCCTTTGTG	CCATGGAGGG	CCGCGAGCCT	GAGCTGGGCG	AGAAGAGAAT	350
TGATGAATTG	CTCGACGCTG	TTGATAGCTG	GATCCCTACG	CCGCAACGTG	400
ATACGGAAAA	ACCCTTCCTA	ATGTCCATTG	AGGAAGTGTT	CTCCATCTCC	450
GGTCGTGGAA	CCGTTGCCTC	CGGCCGTGTT	GAGCGTGGTG	TCCTCAAGAA	500
GGATTCCGAA	GTCGAGCTTG	TTGGCGGCGG	CGTCGCCCCA	ATCAGGACCA	550
AGGTAACCGA	TATCGAAACC	TTCAAGAAGT	CCTGCGACGA	GTCCAGGGCT	600
GGAGACAACT	CTGGCCTTTT	GTTGCGTGTT	GTCAAGCGTG	AGGATATCCG	650
CCGTGGTATG	GTCGTTGTCG	TTCTTGGCAG	CGTCAAGGCC	CACGACAAGT	700
TCTTGGTGTC	CATGTATGTT	CTGACCGAAG	CCGAGGGTGG	TCGCCGAACT	750
GGATTTCGGCC	AAAACATATC	TCCTCAAATG	TTTATCCGCA	CAGCTGGTAC	800
GTAACGTATA	ATGCCTCTCC	TCTTCATATA	TACCACCCCC	CCCACCACTG	850
ACTCCCTGAC	TCTTCGATTA	CAGACGAGGC	CGCCGATCTC	AGCTTCCCTG	900
ACGCAGCAGA	CGAAACCAAA	CTGTTATGTC	CCGGTGACAA	CGTCGAGATG	950
ATCCTCAAGA	CACACCGCCC	CATAGCTGCC	GAAG		984

2) INFORMATION FOR SEQ ID NO: 2196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Exserohilum rostratum*
- (B) STRAIN: WSA-215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2196

GCCGCCTCTG	ACGGCCAAAT	GCCCCAGACC	CGTGAGCACT	TGCTGCTTGC	50
TCGCCAGGTC	GGTGTTTACA	AGATTGTTGT	TTTTGTCAAC	AAGGTCGATG	100
CCGTCGAGGA	CAAGGAGATG	TTGGAGCTCG	TTGAGATGGA	GATGCGTGAG	150
TTGCTCAGCA	GCTATGGCTT	CGAGGGCGAT	GAGACTCCCA	TTGTCATGGG	200

CTCCGCTCTC	TGCGCCATCG	AGGGCCGTGA	GCCCGAAATT	GGTGTCAACC	250
GTATTGATGA	GCTGCTCGAG	GCTGTCGACA	CCTGGATCCC	CACCCCTCAG	300
CGTGATACCG	ACAAGCCCTT	CCTCATGGCT	GTTGAGGACG	TCTTCTCCAT	350
TGCTGGCCGT	GGTACCGTCG	TTTCTGGCCG	TGTCGAGCGA	GGTGTCTTGA	400
AGCGCGATGC	CGAAGTCGAG	CTGGTTGGCA	AGGGCACTGC	GCCCATCAAG	450
ACCAAGGTTA	CCGACATTGA	AACCTTCAAG	AAGTCGTGTG	AAGAGTCTCG	500
CGCCGGTGAC	AACTCGGGTC	TCCTCCTCCG	TGGTGTCAAG	CGTGACGACG	550
TCCGCCGTGG	CATGGTCGTT	TCTGTTCTTG	GACAAGTCAA	GGCCCACAAG	600
AAGTTCCTCG	TCTCCATGTA	TGTGTTGAGC	AAAGAGGAAG	GTGGCCGCCA	650
CACGGGCTTC	GGCGAGAACT	ACAGGCCACA	AATGTTTCATC	CGTACTGCTG	700
ACGAGTCATG	CGCGCTGCAC	TGGCCAGAAG	GTACCCCAAG	TGCTCACGAC	750
AAGCTTGTTA	TGCCTGGTGA	TAACGTTGAG	ATGGTTTGTG	AGCTTCACGT	800
GCCACA					806

2) INFORMATION FOR SEQ ID NO: 2197

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium moniliforme*
- (B) STRAIN: WSA-213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2197

ACCCGTGAAC	ACTTGCTCCT	CGCTCGTCAG	GTTGGTGTTC	AGCGAATTGT	50
CGTCTTTGTC	AACAAGGTCG	ATGCCATTGA	TGACCCCGAG	ATGCTTGAGC	100
TCGTCGAGAT	GGAGATGCGC	GAGCTTCTTA	ACACCTATGG	CTTCGAAGGC	150
GACGACACTC	CCGTCAATCAT	GGGCTCGGCT	CTCATGTCTC	TCCAGAACCA	200
GCGCCCTGAG	ATTGGCACCG	AGAAGATTGA	TGAGCTTCTT	GCTGCCGTCG	250
ACGAGTGGAT	CCCAACCCCC	GAGCGTGACC	TTGACAAGCC	CTTCCTTATG	300
TCCGTCGAGG	ATGTCTTCTC	CATTGCTGGC	CGTGGTACCG	TCGTGTCTGG	350
CCGTGTGGAG	CGTGGTGTTC	TGAAGCGTGA	CCAGGAGATC	GAGCTTGTTG	400
GAAAGGGTCA	GGAGGTTATC	AAGACCAAGG	TTACCGACAT	CGAGACCTTC	450
AAGAAGTCTT	GTGAGCAGTC	CCAGGCTGGT	GACAACTCTG	GTCTCCTCAT	500
CCGAGGTGTT	CGCCGTGAGG	ATGTCCGCCG	TGGTATGGTC	GTCTGCGCTC	550
CTGGCACCGT	GAAGTCTCAC	ACCCAGTTCC	TCGCTTCCCT	CTATGTCCTC	600
TCCAAGGAGG	AGGGTGGCCG	ACACACCGGT	TTCCAGGAGC	ACTACCGACC	650
CCAGCTCTAC	CTCCGAACCG	CAGATGAGTC	CATTGACCTG	ACTTTCCCTG	700
AGGGTACTGA	GGATGCCTCC	AGCAAGATGG	TCATGCCTGG	CGACAACACC	750
GAGATGGTTG	TCACCATGGG	TCACCCCAAT	GCCATCGAGG	TTGGTCAGC	799

2) INFORMATION FOR SEQ ID NO: 2198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium solani*
(B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2198

CTCTGACGGT	CAGATGCCCC	AGACCCGTGA	GCACTTGCTG	CTTGCCCGTC	50
AGGTCGGTGT	CCAGAAGATT	GTCGTCTTCG	TCAACAAGGT	CGATGCCATT	100
GACGACCCCTG	AGATGCTTGA	GCTCGTCGAG	ATGGAGATGC	GTGAGCTCCT	150
CAACACCTAC	GGCTTCGAGG	GTGACGAGAC	CCCTGTCATC	ATGGGCTCTG	200
CTCTCATGTC	CCTCCAGAAC	CAGCGCCCCG	AGATCGGTAG	CCAGAAGATT	250
GACGAGCTCC	TTGCCGCCGT	TGACGAGTGG	ATCCCTACCC	CCGAGCGTGA	300
CCTTGACAAG	CCCTTCCTCA	TGTCCGTTGA	GGATGTCTTC	TCCATTGCCG	350
GCCGTGGTAC	CGTCGTCTCT	GGCCGTGTCG	AGCGTGGTGT	CCTGAAGCGC	400
GACCAGGAGA	TTGAGCTCGT	CGGCAAGGGT	AACGAGGTCA	TCAAGACCAA	450
GGTCACCGAC	ATTGAGACCT	TCAAGAAGTC	TTGCGAGCAG	TCCAGGCTG	500
GTGACAACTC	TGGTCTCCTC	ATCCGAGGTG	TCCGCCGTGA	GGATGTCCGC	550
CGTGGTATGG	TCGTCTGCGC	CCCCGGCACT	GTCAAGTCCC	ACACTCAGTT	600
CCTTTCTTCC	CTCTACGTCC	TCACCAAGGA	GGAGGGTGGC	CGACACACTG	650
GCTTCCAGGA	GCACTACCGA	CCCCAGCTCT	ACCTCCGAAC	TGCTGATGAG	700
TCCATCGACC	TGACCTTCCC	CGAGGGTACC	GAGGACGCCA	GCAGCAAGAT	750
GGTCATGCCC	GGTGACAACA	CCGAGATGGT	CATCACCATG	GGCCACCCCA	800
ACGCCATTGA	GGTCGGTCA				819

2) INFORMATION FOR SEQ ID NO: 2199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1025 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Histoplasma capsulatum*
(B) STRAIN: WSA-377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2199

TGCTGACGGC	CAAATGTAAG	ACGCCGCGAG	GGAGTGCTGA	AGGTTTTATG	50
CTTTTTAGGC	CCTTTGTTTC	TGAGAGCATG	ATGATACTAA	TACTCGGAAA	100
CGTATCTATT	AGGCCTCAAA	CACGTGAGCA	TTTGCTCCTT	GCCCGACAGG	150
TCGGTGTCCA	AAAGATCGTC	GTTTTTCGTGA	ACAAAGTCGA	CGCCCTTGAG	200
GACAAGGAGA	TGTTGGAGCT	TGTCGAGTTA	GAAATGAGAG	AGCTCTTAAA	250
CACCTACGGA	TTTGAGGGTG	AAGAGACACC	CATCATCTTT	GGTTCTGCCC	300
TTTGCGCCAT	GGAAGGCCGT	GAGCCTGAGT	TGGGAGAAAA	GAAAATTGAT	350
GAATTGCTGG	AGGCTGTTGA	TACTTGATC	CCAACACCAC	AACGTGATAC	400
CGAAAAACCT	TTCTTGATGT	CCGTTGAGGA	AGTATTCTCT	ATCTCCGGTC	450
GTGGAACCGT	TGCCTCCGGT	CGTGTTGAGC	GCGGTGTCCT	CAAGAAGGAT	500

TCAGAAGTCG	AGCTAATTGG	GGGCGGCTCC	ACCCCCATCA	GGACGAAGGT	550
AACTGATATC	GAAACTTTCA	AGAAATCCTG	TGACGAGTCT	AGAGCTGGGG	600
ACAACTCCGG	TCTTTTATTG	CGTGGTATCA	AGCGTGAAGA	TATCCGCCGT	650
GGTATGGTAG	TTGCCGTTCC	TGGCAGCGTC	AAGGCCCACG	ACAAGTTCTT	700
GGTGTGATG	TATGTCCTGA	CCGAAGCTGA	GGGTGGTCGC	CGAACCGGAT	750
TCGGCCAGAA	CTATCGTCCT	CAAATGTTCA	TCCGCACAGC	TGGTATGTCA	800
AAATGGGGCC	CCTTTTCATA	ATCCTTTCTT	TTTTTCCTTT	TCCTCTCTCT	850
ATCTCTCTCT	CTGTTTCTTT	TCAACTCGCC	TGATTCACGA	AATTAATAA	900
CCCCTTTGAT	TATAGACGAA	GCCGCCCATC	TCAGCTTCCC	TAGTGGAGCA	950
GATGAAAGCA	AACTCGTTAT	GCCTGGTGAC	AACGTCGAGA	TGATCCTCCA	1000
GACACACCGC	CCCGTGGCTG	CTGAG			1025

2) INFORMATION FOR SEQ ID NO: 2200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kocuria kristinae*
- (B) STRAIN: ATCC 27570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2200

AGCACGTGCT	GCTCGCCCGC	CAGGTCGGCG	TGCCGACCCT	GCTGGTCGCC	50
CTGAACAAGG	CCGACATGGT	CGAGGACGAG	GAGCTGCTGG	ACCTCGTCGA	100
GATGGAGGTC	CGCGAGCTGC	TGTCCTCCCA	GGAGTTCGAC	GGCGACAACG	150
CCCCCGTCAT	CCGCGTCTCC	GCGCTGAAGG	CGCTGGAGGG	CGACGAGAAG	200
TGGGTCAAGT	CCATCGAGGA	GCTCATGGAG	GCCGTGGACG	AGTACATCCC	250
GGACCCCGTG	CGCGACAAGG	ACAAGCCGTT	CCTGATGCCC	ATCGAGGACG	300
TCTTCACCAT	CACCGGGCGC	GGCACCGTGG	TGACCGGTCG	CGCCGAGCGC	350
GGGACCCTGG	CCCTGAACTC	CGAGGTCGAG	ATCGTCGGCA	TCCGCCCGAT	400
CCAGAAGACC	ACGGTCACCG	GGATCGAGAT	GTTCCACAAG	CAGCTCGACG	450
AGGCCTGGGC	CGGCGAGAAC	TGCGGTCTGC	TGCTGCGCGG	CCTGAAGCGC	500
GACGACGTCG	AGCGCGGCCA	GGTCGTGGTG	AAGCCGGGTT	CCATCACCCC	550
GCACACCAAC	TTCGAGGCGA	ACGTCTACAT	CCTGTCCAAG	GACGAGGGTG	600
GGCGTCACAA	CCCGTTCTAC	TCGAACTACC	GTCCGCAGTT	CTACTTCCGG	650
ACCACCGACG	TCACCGG				667

2) INFORMATION FOR SEQ ID NO: 2201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Vibrio mimicus*

(B) STRAIN: ATCC 33653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2201

TGCTGCAACA	GATGGTCCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTGCTGG	50
GTCGCCAAGT	AGGTATTCCT	TACATCATCG	TATTCATGAA	CAAATGTGAC	100
ATGGTTGACG	ATGAAGAGCT	TCTAGAGCTG	GTTGAGATGG	AAGTTCGTGA	150
GCTTCTGTCT	GAGTACGATT	TCCCAGGTGA	TGACCTGCCA	GTAATCCAAG	200
GTTCAGCACT	AGGCGCGCTA	AACGGCGAAG	CACAGTGGGA	AGCGAAGATT	250
GTTGAACTAG	CAGAAGCACT	AGATTTCATAC	ATTCCAGAGC	CAGAGCGTGC	300
AGTAGACATG	GCATTCCTGA	TGCCAATCGA	AGACGTATTC	TCAATCCAAG	350
GTCGTGGTAC	AGTAGTAACT	GGCCGTATCG	AGCGCGGCAT	CCTGAAAGTG	400
GGTGACGAAG	TTGCGATCGT	TGGTATCAAA	GACACAGTAA	AAACTACCTG	450
TACAGGTGTA	GAAATGTTCC	GTAAGCTGCT	TGACGAAGGT	CGTGCAGGTG	500
AGAACGTTGG	TGCACTGCTA	CGTGGTACTA	AGCGTGAAGA	AGTAGAGCGT	550
GGTCAAGTAC	TGGCGAAGCC	AGGTTCAATC	ACCCACACA	CTAAGTTCGA	600
ATCAGAAGTA	TACGTACTGT	CAAAAGACGA	AGGTGGCCGT	CATACTCCAT	650
TCTTCAAAGG	TTACCGTCCA	CAGTTCTACT	TCCGTACAAC	TGACGTAACA	700
GGCAGCATCG	AGCTTCCAGA	AGGCGTAGAA	ATGGTAATGC	CAGGCGACAA	750
CATCAAGATG	GTTGTAGACC	TGATTGCA			778

2) INFORMATION FOR SEQ ID NO: 2202

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter freundii*

(B) STRAIN: ATCC 8090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2202

AACGCTGACC	CTGCAGGTTA	TTGCCGCTGC	GCAGCGTGAA	GGTAAAACCT	50
GTGCATTTAT	CGATGCAGAA	CACGCACTGG	ACCCGGTCTA	TGCCCCGTAAG	100
CTTGCGGTTG	ATATCGATAA	CCTGCTGTGT	TCTCAGCCGG	ATACCGGTGA	150
ACAAGCGCTG	GAAATCTGTG	ATGCACTGGC	GCGCTCCGGT	GCGGTTGACG	200
TTATCGTTGT	CGACTCCGTT	GCCGCATTGA	CGCCGAAGGC	AGAAATCGAA	250
GGCGAGATTG	GCGACTCTCA	CATGGGCCTT	GCGGCGCGTA	TGATGAGCCA	300
GGCGATGCGT	AAGCTGGCCG	GTAACCTGAA	GCAGTCCAAC	ACGCTGCTGA	350
TTTTTCATCAA	CCAGATCCGT	ATGAAGATTG	GCGTTATGTT	CGGTAACCCG	400
GAAACCACCA	CC				412

2) INFORMATION FOR SEQ ID NO: 2203

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
- (B) STRAIN: 20:1.2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2203

TTTAGATCCA	TCTTATGCTA	GAAATTTAGG	TGTTGATATA	GATAACCTAA	50
TAGTTTCTCA	ACCAGATACA	GGAGAACAGG	CTTTAGAGAT	AACAGAAGCT	100
TTAGTAAGAT	CAGGAGCAGT	AGATGTTATA	GTTGTAGACT	CTGTAGCAGC	150
TTTAGTTCCT	AGGGCAGAAA	TAGAAGGAGA	AATGGGAGAC	TCACATGTAG	200
GTCTTCAAGC	AAGACTTATG	TCTCAAGCCC	TAAGAAAATT	AGCAGGATCT	250
ATAAATAAAT	CTAAGTGTGT	AGCTATATTT	ATAAACCAAT	TAAGAGAAAA	300
GGTTGGTATA	ATGTTTGGAA	ATCCAGAAAC	AACTCCT		337

2) INFORMATION FOR SEQ ID NO: 2204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Francisella tularensis*
- (B) STRAIN: ATCC 29684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2204

AAAGCAAGGC	GGTACTGCAG	CATTTGTTGA	TGCTGAGCAT	GCACTAGATC	50
CAAAATATGC	AAAGCTTTTA	GGTGTGATG	TTGATAATCT	GATCGTGTCA	100
CAGCCGGATA	CGGGTGAGCA	AGCTTTAGAG	ATTGCTGATA	TGTTGGTACG	150
TTCTGGAGGA	GTTGATATTG	TAGTAATTGA	CTCTGTTGCT	GCACTTACGC	200
CAAAGGCAGA	GATTGAGGGT	GACATGGGCG	ACTCGCACAT	GGGCTTACAA	250
GCAAGATTAA	TGTCACAAGC	ACTAAGAAAA	CTAACGGCAA	ATATCAAGCG	300
CTCAAATACT	CTAGTGATAT	TCATTAACCA	AATTCGTATG	AAGATCGGGG	350
TTATGTTTGG	TAACCCTGAA	ACTACAACCT			379

2) INFORMATION FOR SEQ ID NO: 2205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus anaerobius*

(B) STRAIN: ATCC 27337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2205

ACTTGACCCA	GTATATGCAA	GGGCTCTTGG	AGTGGATATA	GACAACCTAG-	50
TCATATCTCA	GCCAGATACA	GGAGAACAGG	CCCTAGATAT	AGCAGAGTCC-	100
CTTATAAGAT	CAGGAGCTGT	AGATATACTA	GTAATAGACT	CAGTAGCTGC-	150
CCTAGTACCT	AAGGCAGAAA	TAGAAGGTGA	CATGGGAGAT	TCTCACGTAG-	200
GTCTACAGGC	TAGACTTATG	TCACAGGCAC	TTAGAAAATT	GACTGGATCT-	250
ATAAAGAAGT	CAAACGTGTG	TGTTATATTT	ATCAACCAGT	TGAGAGAAAA-	300
AGTAGGGGTT	ATGTTTCGTA	ATCCAGAGAC	AACAACA		337

2) INFORMATION FOR SEQ ID NO: 2206

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Peptostreptococcus asaccharolyticus*

(B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2206

TCTTGATGCT	GGATATGCAA	AAAACCTTGG	AGTAGATGTA	GAAAATTTAA-	50
TTATTTCTCA	ACCTGATACA	GGTGAGCAAG	CCTTAGAAAT	AACTGAAGCT-	100
CTTGTAAGAT	CTAACGCTGT	TGATTTAATT	ATTATAGACT	CAGTTGCCGC-	150
ACTTGTAACCA	AAAGCAGAAA	TCGATGGTGA	CATGGGAGCT	GCACAAATAG-	200
GTCTTCAAGC	AAGACTTATG	TCTCAAGCTC	TTAGAAAATT	AACTGGGGCA-	250
ATCAACAAGT	CAAAATGTAC	CGTTGTATTT	ATTAACCAAC	TTAGAGAAAA-	300
AGTTGGTATC	ATGTTTGGTA	ACCCAGAAAC	TACAACA		337

2) INFORMATION FOR SEQ ID NO: 2207

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 408 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Providencia stuartii*

1135

(B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2207

CTCACGTTGC	AAGTTATTGC	AGCAGCACAA	CGTAGCGGAA	AAACCTGTGC	50
ATTTATCGAC	GCTGAACATG	CGCTAGATCC	AATCTATGCG	AAAAAACTGG	100
GTGTTGATAT	CGATAACCTT	CTATGTTCTC	AACCTGATAC	TGGTGAGCAA	150
GCATTAGAGA	TTTGTGATGC	ACTGACGCGT	TCAGGCGCTG	TTGATGTCAT	200
TATCGTTGAC	TCCGTGGCCG	CATTAAACACC	AAAAGCTGAA	ATTGAAGGTG	250
AAATCGGTGA	CTCACACATG	GGCTTAGCGG	CTCGTATGAT	GAGCCAAGCG	300
ATGCGTAAAT	TAGCGGGTAA	CTTAAAGAAC	TCGAATACAC	TTTTAATCTT	350
CATTAAACAA	ATCCGTATGA	AGATTGGCGT	TATGTTTGGT	AACCCAGAAA	400
CCACTACA					408

2) INFORMATION FOR SEQ ID NO: 2208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Paratyphi A
- (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2208

GCTGCAGGTG	ATTGCCGCTG	CGCAGCGTGA	AGGTAAAACC	TGTGCGTTTA	50
TCGATGCGGA	ACACGCGCTT	GACCCTGTTT	ACGCACGCAA	GCTGGGCGTC	100
GATATCGATA	ACCTGCTTTG	TTCTCAGCCG	GATACCGGCG	AGCAGGCGCT	150
GGAAATCTGT	GACGCGCTGG	CGCGTTCAGG	CGCGGTGGAC	GTCATTGTGG	200
TCGACTCCGT	AGCGGCGCTA	ACGCCGAAAG	CGGAAATCGA	AGGCGAAATT	250
GGCGACTCTC	ACATGGGCCT	CGCGGCGCGT	ATGATGAGCC	AGGCGATGCG	300
TAAGCTGGCG	GGGAACCTAA	AACAGTCCAA	CACGCTGTTG	ATTTTCATCA	350
ACCAGATCCG	TATGAAGATT	GGCGTGATGT	TCGTAACCC	GGAAACCACC	400
ACC					403

2) INFORMATION FOR SEQ ID NO: 2209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*
 serotype Typhimurium
 (B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2209

GACCCTGACG	CTGCAGGTGA	TTGCCGCTGC	GCAGCGTGAA	GGTAAAACCT	50
GTGCGTTTAT	CGATGCGGAA	CACGCGCTTG	ACCCTGTTTA	CGCACGCAAG	100
CTGGGCGTCG	ATATCGATAA	CCTGCTCTGC	TCTCAGCCGG	ATACCGGCGA	150
GCAGGCGCTG	GAAATCTGTG	ACGCGCTGGC	GCGTTCAGGC	GCGGTGGACG	200
TCATTGTGGT	CGACTCCGTA	GCGGCGCTAA	CGCCGAAAGC	GGAAATCGAA	250
GGCGAAATCG	GCGACTCTCA	CATGGGCCTC	GCGGCGCGTA	TGATGAGCCA	300
GGCGATGCGT	AAGCTGGCGG	GGAACCTGAA	ACAGTCCAAC	ACGCTGTTGA	350
TTTTCATCAA	CCAGATCCGT	ATGAAGATTG	GCGTGATGTT	CGGTAACCCG	400
GAAACCACCA	CC				412

2) INFORMATION FOR SEQ ID NO: 2210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
- (B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2210

ATTAGATCCT	GTTTACGCAG	AAGCTTTAGG	CGTAGATATA	CAAAATTTAT-	50
ATTTATCTCA	ACCTGATCAT	GGGGAACAAG	GTTTAGAAAT	TGCCGAAGCA-	100
TTTGTTAGAA	GTGGCGCTGT	TGATATCGTT	GTGGTCGATT	CAGTTGCTGC-	150
GCTTACACCT	AAAGCTGAAA	TTGAAGGTGA	AATGGGAGAT	ACGCACGTTG-	200
GTTTGCAAGC	ACGTCTTATG	TCCAAGCCT	TGAGAAAGCT	TTCCGGTGCA-	250
ATTTCAAAAT	CAAATACAAC	AGCAGTATTT	ATCAACCAAA	TCCGTGAAAA-	300
AGTTGGTGTG	ATGTTTCGGTA	ATCCTGAAGT	TACACCA		337

2) INFORMATION FOR SEQ ID NO: 2211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
- (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2211

GACACTGACA	TTACAGGTTA	TCGCCGCCGC	ACAGCGTGAA	GGCAAAACGT	50
GTGCATTTAT	CGATGCCGAA	CATGCCCTTG	ACCCAATCTA	TGCCAAGAAA	100
TTGGGTGTAG	ATATTGATAA	CCTACTGTGT	TCTCAGCCAG	ATACTGGCGA	150
GCAGGCACTG	GAAATTTGTG	ATGCGCTGAC	TCGCTCTGGT	GCGGTTGACG	200
TTATCATCGT	TGACTCCGTA	GCGGCATTGA	CACCAAAAGC	TGAAATTGAA	250
GGTGAAATTG	GCGATTCTCA	TATGGGCCTT	GCCGCGCGTA	TGATGAGCCA	300
GGCTATGCGT	AAGCTGGCGG	GTAACCTGAA	GAATGCGAAT	ACCTTACTGA	350
TTTTTATCAA	CCAAATCCGC	ATGAAAATTG	GCGTGATGTT	TGGTAACCCA	400
GAAACCACTA	CC				412

2) INFORMATION FOR SEQ ID NO: 2212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2212

CACGCTCACC	TTGCAAACCA	TCGCGGAAAT	GCAAAAACCTG	GGCGGCACCT	50
GCGCGTTTAT	CGACGCCGAG	CACGCACTGG	ACGTACAGTA	CGCGCAAAAG	100
CTGGGCGTCA	ACCTGAGCGA	TCTGCTGATC	TCGCAACCGG	ACACCGGCGA	150
ACAAGCGCTG	GAAATCTGCG	ACGCCCTGGT	GCGTTCCGGT	TCGGTGGACA	200
TGGTCGTGAT	CGACTCGGTC	GCCGCGCTGA	CCCCGCGCGC	CGAGATCGAA	250
GGCGACATGG	GCGATTGCT	GCCAGGTTTG	CAGGCACGTT	TGATGTCGCA	300
AGCACTGCGC	AAGCTTACCG	GTTCGATCAA	CCGCACCAAC	ACCCTGGTCA	350
TCTTCATCAA	CCAGATCCGC	ATGAAAATCG	GCGTCATGTT	CGGCAGCCCG	400
GAAA					404

2) INFORMATION FOR SEQ ID NO: 2213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2213

CGTGCCATTG	ACATGATTTC	CGAAGAAGAC	GCTGAAGGCA	CG
------------	------------	------------	------------	----

42

2) INFORMATION FOR SEQ ID NO: 2214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2214

CAACTACATT ACGTTCTGCA ACACAAGGTC GTGGTACTTT CAGTATGACA	50
TTTGACCACT ATGAAGATGT TCCTAAGAGC ATTGCAGAAG AAATCATCAA	100
GAAAAATGGC GGTAACGGAG AATAA	125

2) INFORMATION FOR SEQ ID NO: 2215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2215

CGACTCAAAT GCGTTCTATG TCTCAAGGTC GTGCGACATA CTCAATGGAA	50
TTTGCTAAAT ATGCTGAAAC TCCACGTAAC GTGGCTGAAG GCATCATCGC	100
TAAATTCCAA GCTGGCGGTA AAAAAGGTGA CGACGAGTAA	140

2) INFORMATION FOR SEQ ID NO: 2216

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
(B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2216

CCGGTGACCT GCGTTCTAAG ACGCAGGGTC GCGCTGTCTA CTCCATGGAG	50
TTCGACAGCT ACGCCGAGGT TCCGCGCGCG GTCGCGGATG AGATCGTCGG	100
CAAGTCTCGG GGCAACTGA	119

2) INFORMATION FOR SEQ ID NO: 2217

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
(B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2217

CGACCGACGT TCGCTCCATG TCCAGGGTC GCGCAAGCTA CTCTATGGAA	50
TTCAAAAAAT ACAACACAGC TCCGGCGCAC ATCGCTGAAA CTGTATCCAA	100
AAAACAAGGC TGA	113

2) INFORMATION FOR SEQ ID NO: 2218

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
(B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2218

GCGACCTGCG TTCCCGTACC CAGGGCCGTG CAAACTACAC CATGATCTTC	50
GACTCCTACG CTGAGGTTCC TACCAACGTG GCAGCTGAGA TCGTGGCAGA	100
GCGCAACGGC ACTGCCTAA	119

2) INFORMATION FOR SEQ ID NO: 2219

1140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
- (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2219

AACTCAGCTG	CGTTCTCTGA	CCAAAGGTCG	TGCATCATAC	ACCATGGAAT	50
TCCTGAAGTA	TGATGATGCG	CCTAACAACG	TTGCTCAGGC	CGTTATTGAA	100
GCCCGTGGTA	AGTAA				115

2) INFORMATION FOR SEQ ID NO: 2220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae pneumoniae*
- (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2220

AACTCAGCTG	CGTTCTCTGA	CCAAAGGTCG	TGCATCATAC	ACCATGGAAT	50
TCCTGAAGTA	TGATGATGCG	CCGAACAACG	TTGCTCAGGC	CGTTATTGAA	100
GCCCGTGGTA	AATAA				115

2) INFORMATION FOR SEQ ID NO: 2221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
- (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2221

CAACTCACCT TCGTTCAGGT ACGCAAGGTC GTGGTGTATA CACTATGCAA	50
TTTGACCACT ATGAAGAAGT TCCTAAATCT ATTGCTGAAG AAATCATTA	100
AGCTAATGGT GGA	113

2) INFORMATION FOR SEQ ID NO: 2222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2222

CGGCGACCTG CGGTCCAAGA CCCAAGGCCG GGCGAACTAC TCCATGGTCT	50
TCGACTCCTA CGCCGAAGTG CCGGCCAACG TGTCGAAGGA GATCATCGCG	100
AAGGCGACGG GTCAGTGA	118

2) INFORMATION FOR SEQ ID NO: 2223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
- (B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2223

CCGGCGACCT GCGGTCCAAG ACGCAAGGCC GGGCGAACTA CTCCATGGTG	50
TTCGACTCGT ACGCCGAAGT TCCGGCGAAC GTGTGAAGG AGATCATCGC	100
GAAGGCGACG GGCGAATAG	119

2) INFORMATION FOR SEQ ID NO: 2224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

1142

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
(B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2224

CGGCGACCTG	CGGTCCAAGA	CTCAAGGCCG	GGCGAACTAC	TCGATGGTGT	50
TCGATTCCTA	CGCCGAAGTG	CCGGCTCAGG	TGTCGAAGGA	GATCATCGCG	100
AAGGCGACTG	GCGAGTGA				118

2) INFORMATION FOR SEQ ID NO: 2225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
(B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2225

CGGAGACTTG	CGGTCGAAGA	CCCAGGGCCG	GGCGAACTAC	TCCATGGTGT	50
TCGACTCCTA	CGCCGAAGTG	CCGGCGCAGG	TGGCGAAGGA	GATTATCGCG	100
AAGGCAACGG	GCGAGTAA				118

2) INFORMATION FOR SEQ ID NO: 2226

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
(B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2226

GACCGACCTG	CGTTCTGCAA	CCCAAGGCCG	CGCTACTTAC	TCTATGGAGT	50
TCAAGAAATA	TTCTGAAGCT	CCTGCCCACA	TAGCTGCTGC	TGTAAGTGAA	100
GCCCGTAAAG	GCTAA				115

2) INFORMATION FOR SEQ ID NO: 2227

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2227

AACTTCATTA CGTTCTAACA CGCAAGGTCG CGGTACTTAC ACAATGTACT	50
TTGACCACTA TGCAGAAGTT CCTAAATCAA TTGCTGAAGA AATCATCAAG	100
AAAAATAAAG GTGAATAA	118

2) INFORMATION FOR SEQ ID NO: 2228

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2228

AACTTCATTA CGTTCTAACA CTCAAGGTCG CGGTACTTAC ACTATGTACT	50
TCGATCACTA TGCAGAAGTT CCAAAATCAA TTGCTGATGA TATCATCAAA	100
AAAAATAAAG GTGAATAA	118

2) INFORMATION FOR SEQ ID NO: 2229

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1630 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
 (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2229

CGTTCAATGC	GTGTTCTAGA	CGGTGCAGTT	ATGGTTTACT	GTGCTGTGGG	50
TGGTGTTTCA	CCTCAGTCTG	AAACCGTTTG	GAGACAGGCT	CAGAAGTACA	100
AGGTTTCTCG	TATTGCTTTC	GTTAATAAGA	TGGACCGTAC	TGGTGCTAAT	150
TTCCTACGTG	TTGTAGAGCA	GATTAAGACC	CGTCTAAAGG	GTAACCTGT	200
TCCTCTAATG	TTACCTATCG	GTAAAGAGGA	CAGCTTTGTT	GGTGTAGTTG	250
ACCTAATCAA	GCGTAAGGCT	ATCGACTGGG	ATGAGGCATC	TCAGGGTATG	300
AAGTTTGAGT	ACGTTGACAT	TCCAGCAGAT	ATGGTTGAGG	AAGTTGAAGA	350
GTGGCGTGCA	AAGCTTGTAG	AAGCAGCTGC	AGAAGCTAAC	GACGAGCTGA	400
TGGATAAATT	CTTCGGTGGT	GAAGAGCTGA	CCGAGGAAGA	GATCAAGGCT	450
GCTCTACGTG	AGCGTACTCT	TCGCAACGAA	ATTATTCCTA	TGTGCTGCGG	500
TTCAGCATTT	AAGAACAAGG	GTGTTTCAGG	AATGCTTGAC	GCTGTTGTTG	550
AGTATCTTCC	ATCTCCAGCA	GATGTTTCTG	CTGTTGAGGG	TAAGACCCTA	600
ACCGGTGAAG	CTGATACTCG	TAAGGCTGAC	GATAAAGAGC	CATTCTCTGC	650
TTTAGCATTT	AAGCTAGCAA	ATGACCCATT	CGTAGGTAAC	TTAACATTCT	700
TACGTTGCTA	CTCAGGCTTT	ATTAAGTCTG	GTGACACTGT	AATGAACCTA	750
GATAAGCAGA	AGCGTGAGCG	TTTCGGCCGT	CTAGTTCAGA	TGCACGCTAA	800
TGCTCGTAAT	GAGGTTAGCG	AGGTTTATGC	AGGTGACATC	GTTGCTGCTA	850
TTGGTCTGAA	GGAAACCGTT	ACCGGTGATA	CCTTATGTGA	CCCAGAGCAT	900
CCAATCATTC	TTGAGTCAAT	CGACTTTGCA	GAGCCAGTTA	TCTCTGTAGC	950
AGTTGAGCCT	AAGACCAAGG	ACGATCAGGA	GAAGATGGCT	CTTGCTTTAC	1000
AGCGTTTAGC	AAAAGAAGAT	CCTTCATTCC	GCGTTCGTAC	AGACGAAGAG	1050
TCTGGCCAGA	CCATTATTTC	TGGTATGGGT	GAGCTTCACC	TAGACATCAT	1100
TGTTGACCGT	CTACGCCGTG	AGTTCAAGGT	TGAGTGTAAT	CAGGGTAAGC	1150
CACAGGTTGC	ATACCGTGAG	ACCATTAAGA	GCAAGGTTGA	ACAGCAAGGT	1200
AAGTTTGCTC	GTCAGTCTGG	TGGTCGTGGT	CAGTACGGTG	ACTGCTGGTT	1250
ACGTATGGAA	CCTCTTGAGC	CAGGTAAGGG	CTACGAATTC	GTGAATGAGA	1300
TTGTTGGTGG	TGTAATTCCT	AAGGAATATA	TCCCTGCAAT	TGATAAGGGC	1350
TGTCAGGAGC	AGATCGCTAA	CGGTGTTCTA	GCTGGTTTCC	CAGTTGTTGA	1400
CATCAAGATC	ACTGTATTCT	ATGGTTCTTA	CCACGAAGTT	GACTCTTCAG	1450
AAATGGCATT	CAAGATTGCT	GCTTCTATGG	CATTCAAAGA	GGGCTTCAAG	1500
AAGGCAAATC	CTGTTCTTCT	AGAGCCTTTA	ATGAAGGTAG	AAGTTGATAC	1550
TCCTGAAGAC	TACATGGGTG	ACGTTATTGG	TGACTTAAAC	CGTCGTCGTG	1600
CTATCGTTGA	AGGCATGGAA	GATGGTCCTA			1630

2) INFORMATION FOR SEQ ID NO: 2230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1662 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tetragenococcus halophilus*
 (B) STRAIN: ATCC 33315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2230

1145

TTGAAGTGCA	ACGTTTCATTG	CGTGTGCTAG	ACGGTTCAGT	TACTGTCTTG	50
GACTCACAAT	CAGGTGTTGA	ACCACAACT	GAAACAGTTT	GGCGTCAAGC	100
AACAGAATAT	CAAGTACCTC	GTATTGTATT	CTGTAATAAA	ATGGATAAGG	150
TTGGCGCAGA	TTTCTTATAT	TCTGTCCGAT	CATTGCATGA	TCGTTTAGAA	200
GCTAATGCAC	AACCTATCCA	ATTGCCAATT	GGTGCTGAAG	ATAACTTTGA	250
AGGTATCATC	GACCTTGTGA	AGATGAAAGC	TGAATTTTAT	AAAGATGATT	300
TAGGGACTAC	TTTCGAAGAA	ACTGAAATCC	CAGATGAATA	TAAAGAAACA	350
GCTCAAGAAT	GGCATAATAA	TTTGGTAGAA	TCTGTAGCTG	ATTTTGTATGA	400
AGATATCATG	ATGAAATACT	TGGAAGGTGA	AGAAATTACA	CCTGAAGAGT	450
TACAAGCAGG	TATTCGTAAA	GCAACATTAT	CTGTTGAATT	TTACCCAGTA	500
TTATGTGGTT	CTGCATTTAA	AAACAAAGGT	GTTCAAATGA	TGTTGGATGC	550
AGTAATTGAT	TACTTGCCTT	CTCCAACCGA	CGTCCCCCA	ATTAAAGGGA	600
TCGATCCGAA	AACAGATGAA	GAAACTGAAC	ATCCTGCTGA	TGATAGTGAG	650
CCTTTTTTCAT	CACTTGCTTT	TAAAGTTATG	TCAGACCCTT	ATGTTGGCCG	700
CTTAACTTTC	TTCCGTGTTT	ATTGAGGTGT	GTTGGATACA	GGTTCTTATG	750
TATTGAATGC	TACTAAGGGT	TCACGTGAAC	GAATTGGTCG	TATTTTGCAA	800
ATGCATGCCA	ATTCTCGTTC	TGAGATCGAT	AAGGTTTATT	CAGGTGACAT	850
TGCAGCTGCT	GTAGGCTTGA	AGAACACTAC	AACAGGGGAT	ACCCTTTGTG	900
ATGAGAAAAA	TCCAGTTATT	TTGGAAACTA	TCAACTTCCC	TGAACCAGTA	950
ATTCAAGTTG	CTGTTGAACC	TAAGTCAAAA	GCTGACCAAG	ATAAAATGAG	1000
CGTAGCACTA	CAAAAACCTG	CAGAAGAAGA	CCCATCTTTT	AAAGTGGAAA	1050
CCAACGCTGA	AACTGGCGAA	ACTGTAATTG	CTGGTATGGG	TGAACCTCAA	1100
TTAGACGTTT	TTATTGACCG	TATGAAGACT	GAATTTAAAG	TGGATGCCAA	1150
TATTGGTGCA	CCACAAGTTT	CTTATCGTGA	AACTTCCGT	TCATCAACTA	1200
AAGCTGAAGG	GAAATTTATC	CGCCAATCTG	GTGGTAGAGG	TCAATACGGT	1250
CACGTATGGG	TTGAATTTAC	TCCAAACGAA	GAAGGAGCAG	GATTCGAATT	1300
TAAAAACTCC	ATTGTTGGTG	GGGTTGTCCC	TCGTGACTAT	ATACCTGCAG	1350
TACAAAAAGG	ACTGGAAGAC	GCCATGGAAA	ATGGTGTGTT	AGCTGGTTAT	1400
CCATTAGTTG	ACGTAAAGGC	AGAACTGTTT	GATGGTTCTT	ACCATGACGT	1450
CGACTCTAAT	GAAACAGCCT	TCCGTATTGC	GGCTTCAATG	TCTCTACGTG	1500
AAGCTGCGAA	AAAGGCAGAT	CCAGTTATTC	TTGAACCGAT	GATGAAAGTA	1550
ACAATTAGTA	TCCCTGAAGA	ATATCTAGGT	GATATTATGG	GACATGTTAC	1600
AGCTCGTCGT	GGTCGTGTTG	AAGGAATGGA	TGCTCACGGT	AATGCACAAA	1650
CTGTAAATGC	GT				1662

2) INFORMATION FOR SEQ ID NO: 2231

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*
- (B) STRAIN: ATCC 10790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2231

AAGTAGAACG	TTCTCTACGT	GTAATTGACG	GTTCTGTTGC	GGTGTTCAGT	50
GCTAAAGGTG	GCGTTGAACC	TCAATCCGAA	ACAGTATGGC	GTCAGGCTTC	100
TAACTACGGC	GTACCTCGTA	TCGCTTATGT	AAATAAGATG	GATACTGTAG	150

GTGCTGACTT	CTTCAACGTA	GTTGACATGA	TGAAAGCTCG	TTTGGGTGCA	200
AATTCCGTA	CTATCCAAGT	ACCAATCGGT	GCTGAAGATA	CTTTCGAAGG	250
CATCATTGAC	TTGATGACTA	TGAAAGCGGA	AATTTATAAA	TCCGATGACG	300
GTAAAGAATA	TGAAATCACT	GATATCCCTG	CTGAATATCA	AGAAGTAGCA	350
GAAGCTCGTC	GCGAAATGAT	GATCGATGCT	ATCGCTGAAA	CAGATGATGA	400
TATCATGATG	AAATATTTGG	AAGGCGAAGA	AATTTCTGTG	GAAGAATTGA	450
AAGCGGCATT	GCGTAAAGCT	GTTATTGCTA	ACCAATTATT	CCCAGTTCTT	500
TGTGGTTCTT	CCTATAAAAA	TAAAGGTGTT	CAAATGTTAT	TGGATGCTGT	550
TATCGATTAC	ATGCCAGCTC	CAATCGACAT	CCCACCTATT	AAAGGTGTTG	600
TTCCTGGTAC	TGAAGAAGAA	ACAACCTCGTC	CTTCTTCCGA	TGAAGAGCCA	650
TTCTCTGCAT	TGGCATTCAA	AATCATGGCT	GACCCTTATG	TTGGTAAATT	700
AGCGTTCTTC	CGTGTGTA	CCGGTACATT	GGAATCTGGC	TCCTACGTTT	750
TCAACTCCAC	TAAAGGTAAA	AAAGAACGTA	TCGGTCGTAT	TCTTCAAATG	800
CACGCTAACT	CCCGTAAAGA	AATCGAACGC	GTATATTCTG	GTGACATCGC	850
TGCGGCGGTT	GGCTTAAAGG	ATACTACTAC	AGGCGACACA	TTGTGTGATG	900
AAAAATCTCC	TGTAATCCTT	GAGTCCATGG	AATTCCTGA	ACCAGTTATC	950
TCCGTTGCTG	TTGAACCTAA	AACAAAAGCT	GACCAAGAAA	AAATGGGTAC	1000
AGCTCTTGCT	CGTTTGGCAG	AAGAAGATCC	TACTTTCAAA	GTTTCGTA	1050
ATGAAGAAAC	AGGTCAA	ATTATCTCTG	GTATGGGCGA	ACTTCACTTG	1100
GATATCATCG	TTGACCGTAT	GAACCGTGAA	TTCAAAGTAG	ATTGTAACGT	1150
AGGTAAACCT	CAAGTAGCAT	ACCGCGAAAC	TATCCGTAAA	GCTGTTAAGG	1200
CTGAAGGTAA	ATTTCGTACG	CAATCTGGTG	GTCGTGGTCA	ATATGGTCAC	1250
TGCTGGTTGG	AATTGATTCC	TCAAGAACCA	GGTGCTGGCT	TCGAGTTTGA	1300
AAACAAGGTT	GTAGGTGGTG	CGATTCTCG	TGAATACATC	GGACCTGTTG	1350
AAAGCGGTGT	TAAAGAAGCT	ATGGAATCCG	GTGTTATCGC	TGGGTACCCT	1400
ATGGTTGATG	TTAAAGTTAT	CGTATTTGAT	GGTTCTTACC	ATGACGTTGA	1450
CTCCAACGAA	ATGGCCTTCA	AAATTGCTGG	TTCTATGGGC	TTCAAAGAAG	1500
GTGCTCGCAA	AGCAGACCCT	GCATTGCTTG	AACCATATAT	GGCTGTAGAA	1550
GTAGACGTTT	CTGAAGAATA	CATGGGCGAC	GTTATCGGTG	ACTTGA	1600
TCGTCTGTTG	CGCATGGACG	GCATGGAAGC	TCGTAATGGT	TCCCAACATA	1650
TC					1652

2) INFORMATION FOR SEQ ID NO: 2232

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
- (B) STRAIN: ATCC 29833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2232

AGTAGAGCGT	TCCATGCGTG	TTCTTGACGG	CGCGGTAATG	GTTTACTGTG	50
CAGTTGGTGG	TGTTTCAGCCA	CAGTCTGAAA	CCGTATGGCG	TCAGGCTAAT	100
AAATATAAAG	TTCCACGTAT	TGCGTTCGTT	AACAAAATGG	ACCGTATGGG	150
TGCGAACTTC	CTGCGCGTAG	TTGGTCAACT	GAAATCTCGC	CTTGGTGCGA	200
ACCCAGTTCC	ACTGCAGTTG	GCAATTGGCG	CAGAAGAAAA	ATTACCCGGT	250
ATTATCGATC	TGGTGAAAAT	GAAAGCGATC	AACTGGAACG	AAGCTGATCA	300
GGGCGTGACC	TTCGAATATG	AAGAAATCCC	TGCTGATATG	GCTGAACTGG	350

CTGCTGAATG	GCACCAGAAT	CTGGTTGAAT	CTGCGGCAGA	AGCGTCTGAC	400
GAGCTGATGG	ACAAATACTT	GGGTGGCGAA	GAGCTGACCG	AAGAAGAAAT	450
CAAGAAAGCT	TTACGTCAAC	GTGTTCTGAA	AAGCGAAATT	ATTCTTGTTA	500
CCTGTGGTTC	TGCGTTTAAA	AACAAAGGCG	TACAGGCAAT	GCTGGATGCG	550
GTTATTGAGT	ACCTGCCTGC	ACCAACTGAC	GTTGAATCAA	TCAACGGCAT	600
CTTGGATGAT	GGCAAAGATA	CTCCGGCTGT	TCGTCAATTCT	GACGACAAAG	650
AGCCGTTTCTC	TGCTCTGGCG	TTCAAAATCG	CTACCGACCC	ATTCGTGGGT	700
AACCTGACGT	TCTTCCGCGT	GTA CTCTGGT	ATTGTTAATT	CCGGTGATAC	750
CGTTCTGAAC	TCAGTGAAAT	CGCAACGTGA	ACGCTTAGGT	CGTATCGTAC	800
AGATGCACGC	TAACAAGCGT	GAAGAGATCA	AAGAAGTTCA	CGCCGGTGAT	850
ATCGCAGCCG	CTATCGGTCT	GAAAGATGTG	ACTACGGGTG	ACACTTTGTG	900
TGACCCGAAT	AATCCGATCA	TCTTGGAACG	TATGGAGTTC	CCAGAGCCGG	950
TAATCTCTGT	TGCTGTTGAA	CCAAAAACCA	AAGCTGACCA	AGAAAAAATG	1000
GGTATGGCTC	TGGGGCGTTT	GGCGAAAGAA	GATCCATCAT	TCCGCGTTTG	1050
GACTGACGAA	GAATCTGGTC	AGACTATCAT	CGCTGGTATG	GGTGAGTTGC	1100
ATTTGGATAT	CCTGGTTGAC	CGTATGCGCC	GCGAATTTAA	CGTGGAAGCA	1150
AACGTCGGTA	AACCTCAGGT	TGCGTACCGT	GAAACTATCC	GCGAAACCGT	1200
TAAGGATGTG	GAAGGTAAGC	ACGCTAAGCA	GTCAGGCGGT	CGTGGTCAGT	1250
ATGGTCATGT	TGTTATCGAC	ATGTCCTCCAT	TGCCACCGGG	TGGTGTTGGG	1300
TATGAATTCG	TCAACGAAAT	CGTTGGTGGT	TCTATTCCTA	AAGAATTCAT	1350
TCCGGCCGTT	GATAAAGGTA	TTCAAGAACA	GCTGAAATCT	GGCCCTCTGG	1400
CAGGTTACCC	AGTTGTTGAC	GTTAAAGTGC	GTCTGCACTA	CGGTTCTTAC	1450
CATGACGTTG	ACTCCTCAGA	ATTGGCATTT	AAATTAGCTG	GTTCTATCGC	1500
CTTTAAAGAA	GGTTTCAAAC	GAGCTAAACC	AGTTCTGCTT	GAGCCAATCA	1550
TGAAGGTTGA	AGTCGAAACC	CCTGAAGATT	ACATGGGTGA	CGTAATGGGC	1600
GACCTGAACC	GTCGTCGCGG	TATC			1624

2) INFORMATION FOR SEQ ID NO: 2233

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1636 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2233

GAACGCTCGA	TGCGCGTGCT	TGACGGTGCT	TGCATGGTTT	ACTGCGCAGT	50
GGGCGGTGTT	CAGCCACAGT	CGGAAACCGT	GTGGCGTCAG	GCTAACAAGT	100
ACAAAGTGCC	ACGTCTGGCC	TTCGTCAACA	AGATGGACCG	TACCGGCGCC	150
AACTTCTTCA	AGGTGTACGA	GCAGATGCGT	GCTCGCCTGA	AGGCCAACCC	200
GGTCCTGATC	CAGATCCCTA	TCGGCGCTGA	AGACAACTTC	AAAGGCGTGA	250
TCGATCTGGT	CAAGATGAAG	GCTATCCTGT	GGGACGAAGC	GTCGCAAGGC	300
ATGAAATTCG	ACTACGTCGA	TATTCCTGCA	GAGCTGGCTG	ATTGCGCCGC	350
CGAGTGCGCG	GAAAAGATGG	TTGAAGCTGC	TGCTGAAGCC	ACCGAAGAGC	400
TGATGAACAA	GTACCTGGAA	GAAGGCGACC	TGACCGAAGC	CGAGATCAAG	450
CAGGCGCTGC	GTACCCGTAC	CATCGCTTCG	GAAATCGTTC	CGATGATGTG	500
CGGTACCGCC	TTCAAGAACA	AGGGCGTACA	GGCCATGCTG	GACGCGGTCA	550
TCGAATACCT	GCCATCGCCA	CTGGACATCG	ACGATGTCGG	CGGTACGGAC	600

GAAGACGACC	AGCCAACCAC	CCGTCGCGCA	GCTGACGACG	AGAAATTCTC	650
GGCGCTGGCC	TTCAAGATCA	TGACCGACCC	GTTCGTCGGT	CAATTGGCCT	700
TCTTCCGCGT	GTACTCGGGC	GCCGTCAATT	CGGGCGACAC	CGTGTACAAC	750
TCGGTCAAAG	GTCGTAAAGA	GCGTCTGGGC	CGTATTCTGC	AGATGCACGC	800
GAATCAGCGC	GAAGAGATCA	AAGAAGTGCG	CGCCGGCGAC	ATCGCCGCTG	850
CGGTTGGCCT	GAAAGACGTG	ACCACGGGCG	AAACCCTGTG	CGATCCGACC	900
GCCATCATCA	CGCTGGAAAA	AATGATCTTC	CCTGAGCCTG	TGATTCAACA	950
GGCAGTCGAG	CCAAAAACCA	AGGCCGACCA	GGAAAAAATG	GGCCTGGCAC	1000
TGAACCGCCT	GGCACAGGAA	GATCCTTCGT	TCCGCGTGAA	GACCGATGAA	1050
GAATCGGGCC	AGACCATCAT	CGGTGGWATG	GGCGAGCTGC	ACCTGGAAAT	1100
TATCGTTGAC	CGCATGAAGC	GCGAATTTCG	CGTGGAAGCA	ACCGTCGGCA	1150
AGCCACAAGT	GGCTTACCGC	GAAACGATCC	GTAACACCTG	CGAAGAATCG	1200
GAAGGCAAGT	TCGTCAAGCA	ATCCGGTGGT	CGTGGTCAAT	ACGGTCACGT	1250
TGTGCTGAAG	ATCGAGCCGC	AAGAACCAGG	CAAGGGCTTC	GAGTTCGTTG	1300
ACGCCATCAA	GGGCGGTACC	GTTCTTCGCG	AGTACATCCC	TGCGGTGGAA	1350
AAAGGCGTGC	GCGGCACCCT	GAACACCGGC	GTGCTGGCTG	GTTACCCGGT	1400
CGTGGACGTC	AAGGTCACGC	TGTTCTTCGG	TTCGTACCAC	GATGTGGACT	1450
CGAACGAAAA	CGCGTTCCAG	ATGGCCGCTT	CGATGGCATT	CAAAGAAGGC	1500
TGCCGCAAAG	CATCGCCAGT	CATTCTGGAG	CCAATGATGG	CTGTGGAAGT	1550
GGAAACGCCG	GAAGACTACG	CCGGTACCGT	GATGGGCGAC	CTGTCTGTC	1600
GCCGCGGTAT	GGTGCAGGGC	ATGGACGAAA	TCCCAG		1636

2) INFORMATION FOR SEQ ID NO: 2234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2234

GGCACGAACG	ATCTTGCCGG	ACGGGCCATC	TTCCATACCT	TCGATCAGGC	50
CACGACGACG	GTTCAGGTCA	CCGATCACGT	CGCCCATATA	GTCTTCCGGA	100
GTCTCGACTT	CTACTTTTCAT	GATCGGTTTCG	AGCAGAACCG	GGTTGGCCTT	150
CATGAAGCCA	GCCTTAAAGG	CCATGGAAGC	AGCGATCTTG	AACGCCAGTT	200
CGGAAGAGTC	GACATCGTGG	TAGGAACCGA	AGTGCAGACG	CACGCCCAGA	250
TCCATAACCG	GATAACCTGC	CAGCGGGCCG	GACTTCAGTT	GCTCGCGGAT	300
ACCCTTGTCA	ACACCCGGGA	TGAACTCACC	AGGAATGACG	CCGCCCTTGA	350
TGTCGTTGAC	GAATTCGTAG	GCTTTGCCTT	CTTCCAGCGG	GTACATGTCTG	400
ATCACAACGT	GACCGTACTG	ACCACGACCA	CCGGAATGCT	TGGCGTGCTT	450
ACCTTCGATA	TCCTTGACGG	TGTTACGAAT	GGTTTCACGG	TAGGCAACCT	500
GCGGCTTACC	TACGTTTCGCT	TCTACCTTGA	ACTCGCGACG	CATACGGTCA	550
ACGATGATGT	CCAGGTGCAG	CTCACCCATA	CCGGCGATGA	TGGTTTGGCC	600
AGACTCTTCG	TCAGTCCATA	CGCGGAAGGA	CGGGTCTTCC	TGAGCCAGAC	650
GGCCCAGAGC	CAGGCCCATC	TTCTCTTGGT	CAGCCTTGGT	TTTCGGCTCA	700
ACTGCGATGG	AGATTACCGG	TTCCGGGAAT	TCCATACGCT	CGAGGATGAT	750
CGGCGCTTTT	TCGTACACAC	GGGTGTCACC	GGTGGTCACG	TCTTTCAGAC	800
CAATGGCGGC	AGCGATGTCTG	CCTGCGCGAA	CTTCTTTGAT	CTCTTCACGC	850

TTGTTGGCGT	GCATCTGAAC	GATACGGCCA	AAACGCTCGC	GCTTCTCTTT	900
AACGGAGTTC	AGCACGGAGT	CACCGGAGTT	AACCACACCG	GAGTAAACGC	950
GGAAGAAGGT	CAGGTTGCCT	ACGAACGGGT	CGGTAGCAAT	CTTGAATGCC	1000
AGAGCAGCAA	ACGGCTCGTC	ATCAGAAGCA	TGACGCTCGT	CTTTGGTCTC	1050
GCCATCCAGC	TTCAGACCGT	CGATGGCTGC	TACGTCGGTC	GGCGCCGGCA	1100
GATAGTCAAC	CACGGCATCC	AGCATGGCCT	GTACGCCCTT	GTTCTTGAAC	1150
GCGGAGCCAC	AGGTAACCAG	GATGATTTCG	TTGTTCAGAA	CACGCTGACG	1200
AAGAGCTTTC	TTGATCTCTT	CCTCGGTCAG	TTCTTCACCA	CCCAGGTATT	1250
TTTCCATCAG	GTCTTCAGAC	GCTTCAGCAG	CGGCTTCAAC	CAGGGTCATG	1300
CGCATTTCTT	GCGCTTTTTC	CAGCAGCTCA	GCCGGGACGT	CTTCGTAATC	1350
GAAGGATACG	CCCTGGTCAG	CTTCGCTCCA	GTTGATGGCT	TTCATCTTGA	1400
CCAGGTCGAT	AACGCCCTTG	AAGTTCTCTT	CTGAACCGAT	GTTCAAGTTC	1450
AGCGGAACCG	GGTTACCTTT	CAGACGGGTC	TTGATGTGCT	CAACGCAGCG	1500
CAGGAAGTTG	GCACCGGTAC	GGTCCATCTT	GTTGACGAAC	GCGATACGGG	1550
GAACCTTGTA	CTTGTTAGCC	TGACGCCATA	CGGTTTCAGA	CTGTGGCTGT	1600
ACGCCACHTA	CGGCACAGTA	CACCATCACG	GCGCCGTCCA	GAACACGCAT	1650
GGAACG					1656

2) INFORMATION FOR SEQ ID NO: 2235

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2235

TCTCCTCCCC	ATTTGATAAC	TACCAAATGA	ACGCTATCGA	CTGGTTATGT	50
CAGTCATAAC	CAGTTGATTT	TTAAGAGAGT	TCTTTGGTAT	AATTACAATC	100
GGTAGATACT	GTTATAGAAT	CTAACAAAC	TCAATTAATA	GGAGGAATCA	150
TTTAA					155

2) INFORMATION FOR SEQ ID NO: 2236

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2236

TCTTTCGATT ACTATAAGCC CTAAC TAATT CTTAGTTAAA AACCAAGTGC	50
TCATGGAGCG ACCCTCCATG AGTAGTTAAT AAAGGAAGAT CATC	94

2) INFORMATION FOR SEQ ID NO: 2237

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2237

GTCCCACCGG GGGTGAGTGG GGGCCGGGCA ATCGGCCCCCT GCGAGCCGCC	50
TCACACACCA GTAATCCCAG TAGGTCTCAT GCCCCATGGG TGTTAAAGTG	100
ACACCTAGCC GTAGGCTGAG AATTCTACC CGAGTCCAGG AGGACGAAAA	150

2) INFORMATION FOR SEQ ID NO: 2238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2238

TTCAGTCCTT TAGGCAAGGA GTTAATTGTC	30
----------------------------------	----

2) INFORMATION FOR SEQ ID NO: 2239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
 (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2239

CAACTAGCCT	CTCGCTTATC	TCCCTATGCA	AAATTTCTAG	TCAGTTACAG	50
GGCATAGGGG	GAGCGTAGGC	GGGGGTAGCG	GCTTGCTGAG	CACTTCCTCT	100
ACATCAAAGG	GAATGTTGAG	CCGGCCGTTA	CCCTGTACGA	TCCCATCTGG	150
TTTCTTCGGT	GGTTTGATAA	ATACCCCGTT	GTGACCCTAG	GATCATGTAA	200
CTGGCACAAT	GTAAATAGCT	GTACTGCCAG	GCTGCCGAAT	TAGCAGTCAG	250
AAATGTACAG	CACTGTCAAC	TCGTGGCTGC	GAAATCGTAG	CCACCACGAA	300
GTCCAGGAGG	ACACACA				317

2) INFORMATION FOR SEQ ID NO: 2240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2240

TCCACAGGAT	TAAAACCTAA	GTCCCGTGCT	CTCTCCTGAG	GGGAGAGCAC	50
TATAGTAAGG	AATATAGCC				69

2) INFORMATION FOR SEQ ID NO: 2241

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2241

TCCACAGGAT	TAAAACCTAA	GTCCCGTGCT	CTCTCCGAAG	GGGAGAGCAC	50
TATAGTAAGG	AATATAGCC				69

2) INFORMATION FOR SEQ ID NO: 2242

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
- (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2242

AACAACAAAG AAGATTAATT GATTTTTTTC GCAACATCAA GTATAACTTT	50
AGTTAGAAGT ATTACTTAGT TTAAATTTAA GCTAAGTAAA AAATAATTAT	100
CGAATTATCG AGGAGGATAT TTAAAA	126

2) INFORMATION FOR SEQ ID NO: 2243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2243

GTGTCAACTC ACTGGCTCGG AGCCGAGCAA TCGGCTCAGC GAAGGCGACG	50
GGTCAGTAGC TACTGGCAGC GGAGTAATCT TGCCGGGTCA TTGGAATGCC	100
TTGGGCGCGG CACAACTGAA AACACCAACA CTGCTTTAAC AAGCACCAAC	150
TAGTCCAGGA GGACACAGAA	170

2) INFORMATION FOR SEQ ID NO: 2244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

1153

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
(B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2244

GGCCGGCAAG CCTGCGAGTA AGCTGACGCG GTTAGCACCG CGGCAAAACC	50
AAGAAAAATC AACACTGCTT TTTTAAGCAC CAACAGTCCA GGAGGACAAC	100
AAA	103

2) INFORMATION FOR SEQ ID NO: 2245

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
(B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2245

GCCGAGCGTT GCGCGTAAGC TAGCTCGGTT ACCACGGCGG CAAAAC TAGA	50
AAAACATCAA CACTGCTTTT ATAAGCACCA ACAGTCCAGG AGGACACAGA	100
A	101

2) INFORMATION FOR SEQ ID NO: 2246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
(B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2246

CCAGCTTCCC GCCCGTGCCG CTACGGTGGC ACAAACCCAA AAAGATCAAT	50
CCTGCTGTAA CCCAGCACCA ACAAGTCCAG GAGGACAAGA A	91

2) INFORMATION FOR SEQ ID NO: 2247

1154

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
- (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2247

TCAGGCAAAT AGGCCGTCTG AAAGGCTGAA ATGATTTTTC AGACGGCATT	50
GTTCTTTAAT CGATCTTTAA TGTAAAGGAA TTAGCTC	87

2) INFORMATION FOR SEQ ID NO: 2248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2248

TATAACTTGT TAAGACTAGC TATGCTAGGT TAAAATACAG GTTGAGCTTA	50
TTTATAAGCT GACATTTTAA TGATTGATT TTTAGGGGTA AATGCATTAT	100
AAAAGAATTA TAAATTCTTT TATGCTACAC TCAATCAATT TTCTTCTCAT	150
GATGGTGAGA AACTATCATG AGAGATAAAT TTGAAATAAC TTTTATTAAG	200
AATAGGAGAG ATTTAATA	218

2) INFORMATION FOR SEQ ID NO: 2249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

1155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2249

TTAAACTTGT	TTTAGCTAGA	ATTTCTAGGT	AAAATACAGC	GTAAGCTTAT	50
TAATTAAGCT	AACATCTTTA	TGAATTGATT	TTTTACTGAA	AATGCATTAT	100
AAATGAATTA	TGAATTCTAA	CAATCATTAT	GTCTCATGAT	GGTGAGAAAC	150
TATCATGAGA	GATAATATTG	AAATAACTTT	TACTAGAATA	GGAGAGATTT	200
AATA					204

2) INFORMATION FOR SEQ ID NO: 2250

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2250

CCGTCGGATG	GTGTCGTATA	CCGCGGAGTC	GCCGACGG	38
------------	------------	------------	----------	----

2) INFORMATION FOR SEQ ID NO: 2251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2251

CGGAGCCGTT	CTCGCTGCGT	TACATGCTGG	TGGCTCCG	38
------------	------------	------------	----------	----

2) INFORMATION FOR SEQ ID NO: 2252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2252

CCACATACAG	TGTCTCTC	18
------------	----------	----

2) INFORMATION FOR SEQ ID NO: 2253

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2253

CATTACCCAA CCGAAAGTA

19

2) INFORMATION FOR SEQ ID NO: 2254

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2254

ACCTGAACAG AGAGAAATG

19

2) INFORMATION FOR SEQ ID NO: 2255

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
 (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2255

ATGGCAAAAG	AAAAATTTGA	CCGTTCAAAA	CCACACGTTA	ACATTGGTAC	50
AATCGGCCAC	GTTGACCACG	GTAAAACAAC	ATTAAGTGCT	GCTATCACAA	100
CTGTTTTAGC	TAAGAAAGGT	TTCGCGCAAG	CTCAAGATTA	CGGTTCAATC	150
GATAAAGCTC	CAGAAGAACG	CGAACGTGGT	ATCACAATCA	ACACTTCTCA	200
CGTTGAGTAC	GAAACAGACA	CTCGTCACTA	TGCTCACGTT	GACTGCCCAG	250
GACACGCGGA	CTACGTTAAA	AAC			273

1157

2) INFORMATION FOR SEQ ID NO: 2256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2256

ATGGCTAAAG	CCAAGTTTGA	ACGTAATAAA	CCACACGTAA	ACGTGGGTAC	50
AATCGGTCAC	GTTGACCATG	GTAAAACAAC	TTTAACTGCT	GCGATTGCAA	100
CAATTTGTGC	AAAAACTTAC	GGCGGTGAAG	CGAAAGATTA	CTCACAAATC	150
GACTCAGCAC	CTGAAGAAAA	AGCACGTGGT	ATTACAATTA	ATACATCACA	200
CGTAGAATAC	GATTCTCCAA	CTCGTCACTA	CGCACACGTT	GACTGCCCAG	250
GCCACGCCGA	CTACGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2257

GTGGCGAAGG	CCAAGTTTGA	GCGCACCAAG	CCGCACGTCA	ACATCGGCAC	50
GATTGGTCAC	GTTGACCACG	GCAAGACGAC	GCTGACGGCA	GCTATCACCA	100
AGGTGCTGCA	TGACAAGTAC	CCCGAACTGA	ACGAGTTCAC	CCCCTTCGAT	150
CAGGTCGACA	ACGCTCCCGA	GGAGCGCGAT	CGTGGCATCA	CGATCAACGT	200
CTCTCACGTT	GAGTACCAGA	CCGAGGCGCG	TCACTACGCG	CACGTTGACG	250
CTCCCGGCCA	CGCCGACTAC	GTCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2258

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases

1158

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2258

GTGGCTAAAG	AAAAATTTGA	TCGTTCCCTA	CCGCACGTCA	ACGTTGGCAC	50
TATCGGTCAC	GTTGACCATG	GTAAAACCAC	TCTGACTGCT	GCTCTGACTC	100
GCGTTTGCTC	CGAAGTATTC	GGTTCCGCAA	TCGTTGATTT	CGATAAAATC	150
GACAGCGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCGCGCA	200
CGTTGAATAC	AACTCGCTGA	TCCGTCACTA	CGCTCACGTT	GACTGCCAG	250
GTCACGCTGA	CTATGTGAAG	AAC			273

2) INFORMATION FOR SEQ ID NO: 2259

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
- (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2259

GTGGCAAAGG	CTAAGTTCGA	GCGTACCAAG	CCGCACGTCA	ACATCGGCAC	50
CATCGGTCAC	GTTGACCACG	GTAAGACCAC	CACCACCGCT	GCTATCACCA	100
AGGTTTTGGC	AGACGCTTAC	CCAGAGCTGA	ACGAAGCTTT	CGCTTTCGAT	150
GCCATCGATA	AGGCACCGGA	AGAGAAAGAG	CGTGGTATTA	CCATCAACAT	200
CTCCCACGTG	GAGTACCAGA	CCGAGAAGCG	CCACTACGCA	CACGTTGACG	250
CTCCAGGTCA	CGCTGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

1159

- (A) ORGANISM: *Enterobacter cloacae*
 (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2260

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTTGGTAC	50
TATCGGCCAC	GTTGACCATG	GTAAAACTAC	CCTGACTGCT	GCAATCACTA	100
CCGTTCTGGC	TAAAACCTAC	GGTGGTTCTG	CTCGTGCATT	CGACCAGATC	150
GATAACGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCTCTCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCACACGTA	GACTGCCCGAG	250
GTCACGCCGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2261

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
 (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2261

GTGTCTAAAG	AAAAATTTGA	ACGTACAAAA	CCGCACGTCA	ACGTTGGTAC	50
TATCGGCCAC	GTTGACCATG	GTAAAACTAC	CCTGACTGCT	GCCATCACTA	100
CCGTTCTGGC	TAAAACCTAC	GGTGGTTCCG	CTCGCGCATT	CGACCAGATC	150
GATAACGCGC	CGGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCTCTCA	200
CGTTGAATAT	GACACCCCGA	CTCGCCACTA	CGCGCACGTA	GACTGCCCGG	250
GCCACGCCGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
 (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2262

ATGGCAAAAG	AAAAATTTGA	CCGCTCTAAA	CCCCATGTTA	ACATTGGTAC	50
TATTGGACAC	GTTGACCATG	GTAAACAAC	TTTAACTGCT	GCAATTACAA	100
					1160

CTGTACTTGC	TAAAAAAGGC	TATGCTGATG	CACAAGCTTA	TGACCAAATT	150
GATGGTGCTC	CAGAAGAAAG	AGAACGTGGA	ATCACAATCT	CTACTGCTCA	200
CGTTGAGTAC	CAAACTGACA	GCCGTCAC TA	TGCACACGTT	GACTGCCCAG	250
GACATGCCGA	TTACGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2263

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2263

GTGGCGAAGG	CGAAGTTCGA	GCGGACGAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	GCTGACCGCG	GCTATCACCA	100
AGGTTCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCCG	CGCGTTCGAC	150
CAGATCGACA	ACGCGCCCGA	GGAGCGTCAG	CGCGGTATCA	CCATCAACAT	200
CTCCACGCTG	GAGTACCAGA	CCGACAAGCG	GCACTACGCT	CACGTCGACG	250
CCCCGGGTCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2264

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonae*
- (B) STRAIN: Mgor-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2264

GTGGCGAAGG	CGAAGTTCCA	GCGGACCAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	TCTGACCGCG	GCTATCACCA	100
AGGTCCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCAA	GGCGTTCGAC	150
CAGATCGACA	ACGCGCCTGA	GGAGCGTCAG	CGCGGTATCA	CGATCAACAT	200
CGCGCACGTG	GAATACCAGA	CCGAGAAGCG	TCACTACGCG	CACGTCGACG	250
CCCCCGGCCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
- (B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2265

GTGGCGAAGG	CGAAGTTCCA	GCGGACCAAG	CCCCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	CCTGACCGCG	GCTATCACCA	100
AGGTCTTGCA	TGACAAGTTC	CCGGACCTGA	ACGAGTCGAA	GGCGTTCGAC	150
CAGATCGACA	ACGCTCCTGA	GGAGCGCCAG	CGCGGTATCA	CGATCAACAT	200
CGCGCACGTG	GAGTACCAGA	CCGAGAAGCG	GCACTATGCA	CACGTCGACG	250
CGCCGGGCCA	CGCCGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2266

GTGGCGAAGG	CGAAGTTCTGA	GCGGACGAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTCAC	GTTGACCACG	GCAAGACCAC	GCTGACCGCG	GCTATCACCA	100
AGGTTCTGCA	CGACAAGTAC	CCGGACCTCA	ACGAGTCGCG	TGCGTTCGAC	150
CAGATCGACA	ACGCTCCCGA	AGAGCGTCAG	CGCGGTATCA	CCATCAACAT	200
CTCCACGTG	GAGTACCAGA	CCGAGAAGCG	GCACTACGCC	CACGTCGACG	250
CTCCTGGTCA	CGCTGACTAC	ATCAAGAAC			279

2) INFORMATION FOR SEQ ID NO: 2267

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

1162

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
 (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2267

ATGGCTAAGG	AAAAATTCGA	ACGTAGCAAA	CCGCACGTAA	ACGTTGGCAC	50
CATCGGTCAC	GTTGACCATG	GTAAAACCAC	TCTGACTGCT	GCTTTGACTA	100
CTATTTTGGC	TAAAAAATTC	GGCGGTGCTG	CAAAAGCTTA	CGACCAAATC	150
GACAACGCAC	CCGAAGAAAA	AGCACGCGGT	ATTACCATTA	ACACCTCGCA	200
CGTAGAATAC	GAAACCGAAA	CCCGCCACTA	CGCACACGTA	GACTGCCCGG	250
GTCACGCCGA	CTACGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2268

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2268

ATGGCAAAAG	AAAAATTTGA	TCGCTCAAAA	GAACATGCCA	ATATTGGTAC	50
TATCGGTCAC	GTTGACCATG	GTAAAACAAC	TTTAACAGCT	GCTATCGCAA	100
CTGTATTAGC	TAAAAATGGT	GACACTGTTG	CACAATCATA	CGATATGATT	150
GACAACGCTC	CAGAAGAAAA	AGAACGTGGT	ATTACAATCA	ATACTGCACA	200
TATCGAATAC	CAAACTGACA	AACGTCACTA	TGCTCACGTT	GACTGCCCGG	250
GACACGCTGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2269

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2269

ATGGCAAAAG	AAAAATTTGA	TCGCTCAAAA	GAACATGCCA	ATATTGGTAC	50
TATCGGTCAC	GTTGACCATG	GTAAAACTAC	TTTAACAGCT	GCTATCGCAA	100
CTGTATTAGC	TAAAAATGGT	GACACTGTAG	CACAATCATA	TGACATGATT	150
GACAACGCTC	CAGAAGAAAA	AGAACGTGGT	ATCACAATCA	ATACTGCACA	200
CATCGAGTAT	CAAACTGACA	AACGTCACTA	TGCTCACGTT	GACTGCCCGAG	250
GACACGCTGA	CTATGTTAAA	AAC			273

2) INFORMATION FOR SEQ ID NO: 2270

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2270

CGATCCTGGT	AGTAGCAGCG	ACTGACGGCC	CGATGCCGCA	GACTCGTGAG	50
CACATCCTGC	TGGGTCGTCA	GGTAGGCGTT	CCGTACATCA	TCGTGTTTCAT	100
GAACAAGTGT	GACATGGTAG	ATGACGAAGA	GCTGCTGGAA	CTGGTCGAGA	150
TGGAAGTTTCG	CGAACTGCTG	TCCGAGTACG	ACTTCCCGGG	TGATGACCTG	200
CCGGTAGTCC	GTGGTTTCYGC	ACTGAAAGCG	CTGGAAGGCG	AAGCTCAGTG	250
GGAAGAGAAG	ATCCTGGAAC	TGGCTGGCCA	CCTGGACACC	TACATTCCGG	300
AGCCCGAGCG	TGCCATCGAC	CTGCCGTTCC	TGATGCCTAT	CGAAGACGTA	350
TTCTCCATCG	CTGGCCGYGG	TACCGTAGTG	ACCGGTCGTG	TAGAGCGCGG	400
TATCGTCAAA	GTTGGTGAAG	AAGTGGAAT	CGTKGGTATC	AAAGATACCA	450
CCAAGACCAC	CTGTACCGGC	GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	500
GGTCGTGCAG	GCGAGAACAT	CGGTGCACTG	CTGCGTGGCG	TGAAGCGTGA	550
AGACGTAGAG	CGTGGTCAGG	TACTGGCCAA	GCCGGGCACC	ATCAAGCCGC	600
ACACCAAGTT	YGAATCTGAA	GTGTACGTGC	TGTCCAAAGA	AGAAGGTGGT	650
CGTCATACCC	CGTTCTTCAA	AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	700
TACCGACGTG	ACCGGTACCA	TCGAACTGCC	GGAAGGCGTA	GAGATGGTAA	750
TGCCGGGCGA	CAACATCAAG	ATGGTTGTTA	CCCTGATTGC	GCCGATCGCG	800
ATGGACGACG	GC				812

2) INFORMATION FOR SEQ ID NO: 2271

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bilophila wadsworthia*

1164

(B) STRAIN: ATCC 49260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2271

CGACGGTCCC	ATGCCCCAGA	CCCGTGAGCA	CATCCTGCTC	GCCCGTCAGG	50
TCGGCGTGCC	TCACCTCGTC	GTGTTTCATGA	ACAAGTGTGA	CCTCGTCGAC	100
GACCCCGAAC	TGCTCGAACT	CGTCGAAATG	GAAGTCCGCG	AACTGCTGAG	150
CTCCTACGGC	TACCCCGGCG	ATGAAATCCC	GGTTGTCCGC	GGTTCCGCTC	200
TGAAGGCTCT	GGAATCCGAT	AGCGCTGATT	CCCCTGACGC	CCAGTGCGTG	250
CTCGAACTGC	TCGCCGCTTG	CGACAGCTAC	TTCCCGGATC	CGGTCCGCGA	300
AACCGACAAG	CCCTTCCTGA	TGCCCATCGA	AGACGTGTTC	TCCATCTCCG	350
GCCGCGGTAC	CGTGGTCACC	GGTCGTGTGG	AACGTGGCAT	CATCAAGGTC	400
GGCGAAGAAG	TCGAAATCGT	GGGTATCCGT	CCCACCGTGA	AGACGACCTG	450
CACCGGCGTC	GAAATGTTCC	GCAAGCTGCT	CGATCAGGGC	CAGGCCGGCG	500
ACAACATCGG	CGCTCTGCTC	CGCGGCACGA	AGCGTGACGA	AGTGGAACGC	550
GGCCAGGTTT	TCGCCGCTCC	CAAGAGCATC	ACGCCCCACA	AGAAGTTCAA	600
GGCTGAAGTG	TACGTTCTGT	CCAAGGAAGA	AGGCGGCCCG	CATACCCCGT	650
TCTTCACCGG	CTATCGTCCT	CAGTTCTACT	TCCGTACCAC	CGACATCACC	700
GGTATCATCG	CTCTTGAAGA	AGGCGTTGAA	ATGGTTATGC	CCGGCGATAA	750
CGCTACCTTT	AATGTCGAGC	TCATTCACCC	CATCGCCATG	GAAAAGGGC	799

2) INFORMATION FOR SEQ ID NO: 2272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevundimonas diminuta*
- (B) STRAIN: ATCC 11568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2272

GATCCTGGTG	TGCTCGGCCG	CTGACGGCCC	GATGCCGCAG	ACCCGCGAGC	50
ACATCCTGCT	GTCGCGTCAG	GTCGGCGTTC	CGGCGCTGGT	GGTGTTCCTG	100
AACAAGGTCG	ACATGGTCGA	CGACGAGGAR	CTGCTGGAGC	TGGTCGAGAT	150
GGAAGTGCGC	GAGCTGCTGA	GCTCGTACCA	GTTCCCGGGC	GACGACATCC	200
CGGTGGTCAA	GGGCTCGGCC	CTGGCCGCGG	TGGAGGATCG	CGACCCGCAC	250
ATCGGCGCCG	AGCGCGTTCT	GGAGCTGATG	GCGGCGGTCG	ACAGCTACAT	300
CCCGCAGCCG	GAACGTCCGA	TCGACATGCC	GTTCCCTGATG	CCGGTGGAAG	350
ACGTGTTCTC	GATCTCGGGC	CGCGGCACCG	TGGTGACGGG	TCGCGTCGAG	400
CGCGGCGTCG	TCAAGGTCGG	TGAAGAAGTC	GAAATCGTCG	GCATCCGTCC	450
GGTTCAGAAG	ACGACCTGCA	CGGGCGTCEA	AATGTTCCGC	AAGCTGCTGG	500
AYCAGGGTCA	RGCCGCGCAC	AACGTGGGCG	TGCTGCTGCG	CGGCACCAAG	550
CGTGAAGACG	TCGAGCGCGG	CCAGGTGCTG	TGCAAGCCGG	GTTCCGATCAC	600
CCCGCACACC	AAGTTCGTGG	CTGAAGCCTA	CATCCTGAAC	AAGGAAGAAG	650
GCGGCCGTCA	CACGCCGTTT	TTCACGAACT	ACCGTCCGCA	GTTCTACTTC	700
CGCACGACGG	ACGTGACCGG	CATCGTGCGC	CTGAAGGAAG	GCGTCGAGAT	750
GATCATGCCG	GGCGACAACG	CCGAGCTGGA	CGTCEA		786

2) INFORMATION FOR SEQ ID NO: 2273

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2273

GCTATTATGG	CTGGATTACT	ATCCAATACG	CTATCCAAGA	ATCCCGTAAC	50
GTACCTGCCG	TCAAATCGCT	GGAAGCAGTC	GGATTAGATA	ATTCATTGAA	100
ATTCCTCAAT	GGCCTTGGTA	TCAATTATCC	TGAGATGCAT	TATTCTAATG	150
CGATTTCAAG	TAATACAAGC	GAATCTGGTA	ACCAATACGG	AGCAAGTAGC	200
GAAAAAATGG	CTGCCGCTTA	CGCTGCCTTT	GCTAATGGCG	GTACATATTA	250
CAAACCGCAA	TACGTCAACC	GAGTTGTCTT	TAGCGACGGT	ACAGAAAAAG	300
TCTTTTCAA	TGGCGGATCA	AAAGCCATGA	AAGAGACGAC	AGCCTACATG	350
ATGACAGACA	TGATGAAGAC	CGTTCCTCAG	TCTGGAACTG	GTACCAATGC	400
TGCAATCCCA	GGAGTTTATC	AAGCAGGTAA	AACTGGTACT	TCCAACATATG	450
CAGATGATGA	GCTAGAGAAG	TTGACAAAAC	CTTATTACAG	TTCTAGCATT	500
GTCACACCAG	ACGAACCTATT	TGTTGGCTAT	ACTCCACAAT	ACTCTATGGC	550
TGTTTGGACA					560

2) INFORMATION FOR SEQ ID NO: 2274

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2274

GCTACTTTGG	AAACATTACT	GTCCAATATG	CTCTTCAACA	ATCACGTAAT	50
GTCACAGCCG	TTGAAACTTT	GAATAAGGTC	GGTCTAGATA	AGGCTAAAGC	100
CTTCCTTAAT	GGGCTTGGTA	TTGATTATCC	AAGCATGCAT	TATGCAAACG	150
CCATTTCAAG	TAATACAAC	GAATCCAACA	AAAAATACGG	TGCAAGTAGT	200
GAAAAAATGG	CTGCTGCCTA	CGCTGCTTTT	GCTAATGGTG	GTATTTACCA	250
CAAGCCAATG	TACATCAATA	AAATCGTCTT	TAGCGACGGT	AGTGAGAAAG	300
AATTTTCTGA	TGCCGGCACA	CGAGCTATGA	AAGAAACTAC	TGCCTATATG	350
ATGACTGAAA	TGATGAAAAC	AGTCCTAGTA	TACGGTACCG	GACGTGGAGC	400
CTACCTACCA	TGGCTTCCAC	AAGCAGGTAA	GACAGGTACT	TCTAACTATA	450

CTGACGACGA	AATTGAAAAG	TATATCAAGA	ACACTGGCTA	CGTAGCCCCA	500
GATGAAATGT	TTGTAGGGTA	TACTCGTAA	TATGCAATGG	CTGTTTGGAC	550
A					551

2) INFORMATION FOR SEQ ID NO: 2275

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2275

GCTATTATGG	CTGGATTACT	ATCCAATACG	CTATCCAAGA	ATCCCGTAAC	50
GTACCAGCCG	TCAAATCGCT	GGAAGCAGTC	GGATTAGATA	ATTCATTGAA	100
GTTCTTCAAT	GGCCTTGGTA	TTAATTACCC	TGAAATGCAT	TATTCTAATG	150
CGATTTCAAG	TAATACAAGC	GAATCTGGTA	ACCAATACGG	AGCAAGTAGC	200
GAAAAAATGG	CTGCCGCTTA	CGCTGCCTTT	GCTAATGGCG	GTACATATTA	250
CAAACCGCAA	TACGTCAACC	GAGTTGTCTT	TAGCGACGGT	ACAGAAAAAG	300
TCTTTTCAAA	TGGCGGATCA	AAAGCCATGA	AAGAAACGAC	AGCCTACATG	350
ATGACAGACA	TGATGAAGAC	CGTTCTTCAA	TCTGGAAGT	GTACCAATGC	400
TGCAATTCCA	GGAGTCTATC	AAGCAGGTAA	AACCGGCACT	TCCAAGTATG	450
CAGATGATGA	ACTAGAGAAG	TTGACAAAAC	CTTATTACAG	TTCTAGCATT	500
GTCACACCAG	ACGAGCTGTT	TGTTGGCTAC	ACTCCACAGT	ACTCTATGGC	550
TGTTTGGACA					560

2) INFORMATION FOR SEQ ID NO: 2276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
- (B) STRAIN: ATCC 35037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2276

TTATTTTGGG	AATATCACCA	TCCAATATGC	GCTCCAACAA	TCACGGAACG	50
TTACAGCCGT	AGAAACCTTG	AACAAAGTCG	GTTTGGATAG	AGCCAAGACC	100
TTCTTGAATG	GAATCGGTAT	TGACTATCCA	GATATGCACT	ATGCCAACGC	150
GATTTCAAGT	AATACGACTG	AGTCAAACAA	AAAGTACGGA	GCAAGTAGTG	200

AGAAAATGGC	TGCTGCTTAC	GCTGCTTTTG	CTAACGGTGG	TATCTACCAT	250
AAACCAATGT	ATATCAACAA	AATCGTCTTT	AGCGATGGTA	GCTCAAAAGA	300
ATACGCTGAT	CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	350
TGACAGAAAT	GATGAAGACT	GTCTTGGCAT	ACGGAACGGG	TCGTGGTGCT	400
TATCTCCCTT	GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACATATAC	450
AGATGATGAA	ATTGAAAAC	ACATCAAAAA	TACTGGTTAT	GTAGCCCCAG	500
ACGAAATGTT	TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	TGTWTGGACA	550

2) INFORMATION FOR SEQ ID NO: 2277

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2277

GCTCCTATCT	GGATTATGCG	ATGTCGGTCA	TTGTTGGCCG	TGCGCTGCCA	50
GATGTCCGAG	ATGGCCTGAA	GCCGGTACAC	CGTCGCGTAC	TTTACGCCAT	100
GAACGTACTA	GGCAATGACT	GGAACAAAGC	CTATAAAAAA	TCTGCCCCGTG	150
TCGTTGGTGA	CGTAATCGGT	AAATACCATC	CCCATGGTGA	CTCGGCGGTC	200
TATGACACGA	TCGTCCGCAT	GGCGCAGCCA	TTCTCGCTGC	GTTATATGCT	250
GGTAGACGGT	CAGGGTAACT	TCGGTTCTAT	CGACGGCGAC	TCTGCGGCGG	300
CAATGCGTTA	TACGGAAATC	CGTCTGGCGA	AAATTGCCCA	TGAACTGATG	350
GCCGAT					356

2) INFORMATION FOR SEQ ID NO: 2278

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2278

CTCTTATCTG	GATTATGCGA	TGTCGGTCAT	TGTTGGCCGC	GCGCTGCCGG	50
ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTGCGGTACT	TTACGCCATG	100
AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAT	CAGCCCGTGT	150
CGTTGGTGAC	GTGATCGGTA	AATACCACCC	GCACGGCGAC	TCCGCGGTAT	200

ATGACACCAT	CGTTCGTATG	GCCCAGCCGT	TCTCGCTGCG	CTACATGCTG	250
GTGGATGGCC	AGGGGAACTT	CGGTTCAATC	GACGGCGACT	CCGCCGCGGC	300
AATGCGTTAT	ACGGAAATCC	GTCTGGCGAA	AATTGCTCAC	GAAGTGA	347

2) INFORMATION FOR SEQ ID NO: 2279

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 43886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2279

AGAGCTCCTA	TCTGGATTAT	GCGATGTCGG	TCATTGTTGG	CCGTGCGCTG	50
CCAGATGTCC	GAGATGGCCT	GAAGCCGGTA	CACCGTCGCG	TACTTTACGC	100
CATGAACGTA	CTAGGCAATG	ACTGGAACAA	AGCCTATAAA	AAATCTGCCC	150
GTGTCGTTGG	TGACGTAATC	GGTAAATACC	ATCCCCATGG	TGACTCGGCG	200
GTCTATGACA	CGATCGTCCG	CATGGCGCAG	CCATTCTCGC	TGCGTTATAT	250
GCTGGTAGAC	GGTCAGGGTA	ACTTCGGTTC	TATCGACGGC	GACTCTGCGG	300
CGGCAATGCG	TTATACGGAA	ATCCGTCTGG	CGAAAATTGC	CCATGAAGTGA	350
ATGGCCGATC	TC				362

2) INFORMATION FOR SEQ ID NO: 2280

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 25922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2280

CTCCTATCTG	GATTATGCGA	TGTCGGTCAT	TGTTGGCCGT	GCGCTGCCAG	50
ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTCGCGTACT	TTACGCCATG	100
AACGTACTAG	GCAATGACTG	GAACAAAGCC	TATAAAAAAT	CTGCCCCGTGT	150
CGTTGGTGAC	GTAATCGGTA	AATACCATCC	CCATGGTGAC	TCGGCGGTTT	200
ATGACACGAT	CGTCCGTATG	GCGCAGCCAT	TCTCGCTGCG	TTACATGCTG	250
GTAGACGGTC	AGGGTAACTT	CGGTTCCATC	GACGGCGACT	CTGCGGCGGC	300
AATGCGTTAT	ACGGAAATCC	GTCTGGCGAA	AATTGCCCAT	GAAGTGAATG	350
CCGATCTC					358

2) INFORMATION FOR SEQ ID NO: 2281

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2281

CCCCCAGCTG GCGGGCGGTA TCGATGGGGG

30

2) INFORMATION FOR SEQ ID NO: 2282

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2282

AGRRGCIMAR ATGTATGA

18

2) INFORMATION FOR SEQ ID NO: 2283

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2283

ATITATGAYG GKITTCAGAG GC

22

2) INFORMATION FOR SEQ ID NO: 2284

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2284

TCTGWGTRAC IGGYTCKGAG A

21

2) INFORMATION FOR SEQ ID NO: 2285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2285

CMCCICCWGG TGGWGAWAC

19

2) INFORMATION FOR SEQ ID NO: 2286

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2286

AGTTGCTGTA TTAGGAAATG

20

2) INFORMATION FOR SEQ ID NO: 2287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2287

TCGAAGTTGC TGTATTAGGA

20

2) INFORMATION FOR SEQ ID NO: 2288

1171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1240 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: BM4339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2288

TAGAAGCTGG	CTCGTTTTTT	TATAAATAAG	TTATTCGTTT	ATTTTTGTTT	50
TGTGCTAAAA	TATGAGAGTA	AATCACTGAA	CGATTTAGAA	TACAGGAGGA	100
CAATCTTTTG	AAGATTACTT	TACTATATGG	CGGACGCAGC	GCAGAGCAGA	150
GCATGAAGTG	TCCATTCTTT	CCGCATTTTC	AGTTTTAAAT	GCCATTTATT	200
ATAATTATTA	CCAAGTTCAA	CTCGTATTTA	TTACAAAAGA	AGGACAATGG	250
GTCAAAGGTC	CATTACTAAC	AGAAAAACCT	GCCAGCAAAG	ATGTCTTGCA	300
TCTTTCATGG	GACCCAAGTG	GACAGACAGA	GGAAGGCTTT	ACAGGAAAAG	350
TGATCAATCC	GGGCGAAATC	AAAGAAGAAG	GAGCCATCGT	TTTTCCAGTT	400
TTACATGGGC	CAAACGGGGA	AGATGGAACG	ATCCAAGGCT	TCTTAGAGAC	450
ATTGAATATG	CCTTATGTCT	GCGCAGGCGT	ATTGACCAGT	GCATGTGCCA	500
TGGATAAAAT	CATGACCAAG	TATATTTTAC	AAGCTGCTGG	TGTGCCGCAA	550
GTTCTTTATG	TACCAGTACT	TAAGAATCAA	TGGAAAGAAA	ATCCTAAAAA	600
AGTATTTGAT	CAATGTGAAG	GTTCTTTGCT	TTATCCGATG	TTTGTCAAAC	650
CGGCGAATAT	GGGTTCTAGT	GTCGGCATTA	CAAAAGCAGA	AAACCGAGAA	700
GAGCTGCAAA	ATGCTTTAGC	AACAGCCTAT	CAGTAGATT	CTCGAGCAAT	750
CGTTGAACAA	GGAATTGAAG	CGCGCGAAAT	CGAAGTTGCT	GTATTAGGAA	800
ATGAAGACGT	TCGGACGACT	TTGCCTGGTG	AAGTCGTAAA	AGACGTAGCA	850
TTCTATGATT	ATGAAGCAAA	ATATATCAAT	AATAAAATCG	AAATGCAGAT	900
TCCAGCCGAA	GTGCCAGAAG	AAGTTTATCA	AAAAGCGCAA	GAGTACGCGA	950
AGTTAGCTTA	CACGATGTTA	GGTGGAAGCG	GATTGAGCCG	GTGCGATTTC	1000
TTTTTTGACAA	ATAAAAATGA	ATTATTCTTG	AATGAATTAA	ACTCTATGCC	1050
AGGATTTACG	GAGTTCAGTA	TGTACCCACT	CTTATGGGAA	AATATGGGCT	1100
TGAAATACGG	TGATTTGATT	GAAGAACTGA	TCCAGTTAGG	AATGAATCGA	1150
TACCATCAGC	GTCAATCTTT	TTTTGAAAAA	AATGAATAAA	GAGAAATAAA	1200
GAAGAGGCTG	GAGTGATTGC	GTAACCGCGT	TCATTCTAGC		1240

2) INFORMATION FOR SEQ ID NO: 2289

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2289

CACCGAAGAA GATGAAAAAA

20

2) INFORMATION FOR SEQ ID NO: 2290

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2290

TGGCACCGAA GAAGATGA

18

2) INFORMATION FOR SEQ ID NO: 2291

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2291

ATTTTGGCAC CGAAGAAGA

19

2) INFORMATION FOR SEQ ID NO: 2292

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2292

GAATCGGCAA GACAATATG

19

2) INFORMATION FOR SEQ ID NO: 2293

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1032 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecium*

(B) STRAIN: BM4147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2293

ATGAATAGAA	TAAAAGTTGC	AATACTGTTT	GGGGGTTGCT	CAGAGGAGCA	50
TGACGTATCG	GTAAAATCTG	CAATAGAGAT	AGCCGCTAAC	ATTAATAAAG	100
AAAAATACGA	GCCGTTATAC	ATTGGAATTA	CGAAATCTGG	TGTATGGAAA	150
ATGTGCGAAA	AACCTTGCGC	GGAATGGGAA	AACGACAATT	GCTATTCAGC	200
TGTACTCTCG	CCGGATAAAA	AAATGCACGG	ATTACTTGTT	AAAAAGAACC	250
ATGAATATGA	AATCAACCAT	GTTGATGTAG	CATTTTTCAGC	TTTGCATGGC	300
AAGTCAGGTG	AAGATGGATC	CATACAAGGT	CTGTTTGAAT	TGTCCGGTAT	350
CCCTTTTGTG	GGCTGCGATA	TTCAAAGCTC	AGCAATTTGT	ATGGACAAAT	400
CGTTGACATA	CATCGTTGCG	AAAAATGCTG	GGATAGCTAC	TCCCGCCTTT	450
TGGGTTATTA	ATAAAGATGA	TAGGCCGGTG	GCAGCTACGT	TTACCTATCC	500
TGTTTTTGT	AAGCCGCGCG	GTTCAGGCTC	ATCCTTCGGT	GTGAAAAAAG	550
TCAATAGCGC	GGACGAATTG	GACTACGCAA	TTGAATCGGC	AAGACAATAT	600
GACAGCAAAA	TCTTAATTGA	GCAGGCTGTT	TCGGGCTGTG	AGGTCGGTTG	650
TGCGGTATTG	GGAAACAGTG	CCGCGTTAGT	TGTTGGCGAG	GTGGACCAAA	700
TCAGGCTGCA	GTACGGAATC	TTTCGTATTC	ATCAGGAAGT	CGAGCCGGAA	750
AAAGGCTCTG	AAAACGCAGT	TATAACCGTT	CCCGCAGACC	TTTCAGCAGA	800
GGAGCGAGGA	CGGATACAGG	AAACGGCAAA	AAAAATATAT	AAAGCGCTCG	850
GCTGTAGAGG	TCTAGCCCGT	GTGGATATGT	TTTTACAAGA	TAACGGCCCGC	900
ATTGTACTGA	ACGAAGTCAA	TACTCTGCCC	GGTTTCACGT	CATACAGTCG	950
TTATCCCCGT	ATGATGGCCG	CTGCAGGTAT	TGCACTTCCC	GAAGTGAATTG	1000
ACCGCTTGAT	CGTATTAGCG	TTAAAGGGGT	GA		1032

2) INFORMATION FOR SEQ ID NO: 2294

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2294

AAACGAGGAT GATTTGATTG

20

2) INFORMATION FOR SEQ ID NO: 2295

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

1174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2295

TTGAGCAAGC GATTTCGG

18

2) INFORMATION FOR SEQ ID NO: 2296

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: V583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2296

ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	50
TGATGTGTCG	GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	100
AAAAATTCGA	TCCGCACTAC	ATCGGAATTA	CAAAAAACGG	CGTATGGAAG	150
CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	GCCGATAGTC	TCCCCGCCAT	200
ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTCATG	AAAGAAAGAG	250
AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCCCGGTTT	GCATGGCAAA	300
TGCGGGGAGG	ATGGTGCGAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	350
CTATGTAGGC	TGCGATATTC	AAAGCTCCGC	AGCTTGCATG	GACAAATCAC	400
TGGCCTACAT	TCTTACAAAA	AATGCGGGCA	TCGCCGTCCC	CGAATTTCAA	450
ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	AGGACGCTTA	CCTACCCTGT	500
CTTTGTGAAG	CCGGCACGGT	CAGGTTCTGC	CTTTGGCGTA	ACCAAAGTAA	550
ACAGTACGGA	AGAACTAAAC	GCTGCGATAG	AAGCAACAGG	ACAATATGAT	600
GGAAAAATCT	TAATTGAGCA	AGCGATTTTC	GGCTGTGAGG	TCGGCTGCGC	650
GGTCATGGGA	AACGAGGATG	ATTTGATTGT	CGGCGAAGTG	GATCAAATCC	700
GGTTGAGCCA	CGGTATCTTC	CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	750
GGCTCAGAGA	ATGCGATGAT	TATCGTTCCA	GCAGACATTC	CGGTGAGGA	800
ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	GTGCTTGAT	850
GCAGAGGGCT	TGCTCGTGTT	GATCTTTTTT	TGCAGGAGGA	TGGCGGCATC	900
GTTCTAAACG	AGGTCAATAC	CCTGCCCGGT	TTTACATCGT	ACAGCCGCTA	950
TCCACGCATG	GCGGCTGCCG	CAGGAATCAC	GCTTCCCGCA	CTAATTGACA	1000
GCCTGATTAC	ATTGGCGATA	GAGAGGTGA			1029

2) INFORMATION FOR SEQ ID NO: 2297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

WO 01/23604

PCT/CA00/01150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2297

TTCAGGAGGG GGATCGC

17